

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 12:56:17 ; Search time 23 Seconds

(without alignments)
484.580 Million cell updates/sec

Title: US-09-862-802-2

Sequence: 1 MTSEITYAEVRFKFEKSSG.....NDVNCIGPQKRCVCEMKIHL 237

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	251	19.6	301	1	LEC1_MOUSE
2	232	18.1	301	1	LEC1_RAT
3	228.5	17.9	283	1	LEC1_RAT
4	227.5	17.8	306	1	MMGL_RAT
5	224	17.5	207	1	LEC1_CHICK
6	223.5	17.5	311	1	LEC1_HUMAN
7	220.5	17.2	290	1	LEC1_HUMAN
8	218	17.0	283	1	LEC1_HUMAN
9	216.5	16.9	304	1	MMGL_MOUSE
10	213	16.6	548	1	KUCR_MOUSE
11	208.5	16.3	331	1	FCE2_MOUSE
12	196	15.3	550	1	KUCR_RAT
13	187	14.6	1268	1	PGCN_MOUSE
14	184	14.4	1257	1	PGCN_RAT
15	184	14.4	1321	1	PGCN_HUMAN
16	183.5	14.3	2124	1	PGCA_RAT
17	181	14.1	2364	1	PGCA_BOVIN
18	176	13.8	2109	1	PGCA_CHICK
19	176	13.8	2132	1	PGCA_MOUSE
20	176	13.8	2415	1	PGCA_HUMAN
21	175.5	13.7	155	1	PLC_HALLA
22	175.5	13.7	220	1	NK14_MOUSE
23	175	13.7	216	1	NK14_MOUSE
24	175	13.7	2333	1	PGCA_CANFA
25	174	13.6	173	1	LIT2_MOUSE
26	171.5	13.4	1456	1	MANR_HUMAN
27	171	13.4	266	1	KLR3_MOUSE
28	170	13.3	223	1	NK12_MOUSE
29	168	13.1	173	1	LEC2_MEGRO
30	168	13.1	883	1	PGCB_MOUSE
31	168	13.1	3562	1	PGCV_CHICK
32	167	13.0	163	1	ANP_HUMAN
33	167	13.0	216	1	NKGD_HUMAN

34	167	13.0	912	1	PGCB_BOVIN	Q28062	bos taurus
35	165.5	12.9	321	1	FCE2_HUMAN	P06724	homo sapien
36	165	12.9	883	1	PGCB_RAT	P55068	rattus norv
37	164	12.8	223	1	NK13_RAT	P27471	rattus norv
38	162.5	12.7	227	1	NK11_MOUSE	P27811	mus musculus
39	159.5	12.5	162	1	LEC3_MEGRO	P07439	megabalanus
40	158	12.3	233	1	NKGA_MACMU	Q9m233	macaca mula
41	157.5	12.3	179	1	CD94_MACMU	Q9m2K9	macaca mula
42	155	12.1	165	1	LIT1_MOUSE	P43137	mus musculus
43	155	12.1	266	1	KLR5_MOUSE	Q60652	mus musculus
44	154	12.0	179	1	CD94_HUMAN	O13241	homo sapien
45	154	12.0	2738	1	PGCV_RAT	Q9etb4	rattus norv

ALIGNMENTS

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RESULT 1
LEC1_MOUSE          STANDARD;          PRT;          301 AA.
ID  LEC1_MOUSE
AC  P24721:
DT  01-MAR-1992 (Rel. 21, Created)
DT  01-MAR-1992 (Rel. 21, Last sequence update)
DT  30-MAY-2000 (Rel. 39, Last annotation update)
DE  Asialoglycoprotein receptor 2 (Hepatic lectin 2) (MHL-2) (ASGP-R)
DE  (ASGP-R).
GN  ASGR2 OR ASGR-2
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N. A.
RC  STRAIN=C57BL/6; TISSUE=Liver;
RX  MEDLINE=91027942; PubMed=223888;
RA  Sanford J.P., Doyle D.;
RT  "Mouse asialoglycoprotein receptor cDNA sequence: conservation of
RT  receptor genes during mammalian evolution.";
RL  Biochim. Biophys. Acta 1087:259-261(1990).
CC  -1- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO
CC  WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX
CC  CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES
CC  TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE UNITS. AFTER LIGAND
CC  BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AND
CC  TRANSFERRED TO A SORTING ORGANELLE WHERE RECEPTOR AND LIGAND ARE
CC  DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
CC  SURFACE.
CC  -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC  -1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN HEPATIC PARENCHYMAL
CC  CELLS.
CC  -1- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
CC  -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: X53042; CA37211.1; -
DR  PIR: S13165; S13165.
DR  HSSP: P06734; HHLI.
DR  MGD: MGI:88082; Asgr2.
DR  InterPro: IPR002353; Antifreeze2.
DR  InterPro: IPR001304; Lectin_C.
DR  InterPro: IPR005640; lectin_N.
DR  Pfam: PF00059; lectin_C; 1.
DR  Pfam: PF03954; lectin_N; 1.
DR  PRINTS: PR00356; ANTIFREEZE2.1.
DR  SMART: SM00034; CLCT; 1.
DR  PROSITE: PS00615; C_TYPE_LECTIN_1; 1.

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DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
 KW Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
 KM Calcium; Signal-anchor; Phosphorylation.
 FT DOMAIN 1 58 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 59 79 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 80 301 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 169 295 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 170 181 BY SIMILARITY.
 FT DISULFID 198 293 BY SIMILARITY.
 FT DISULFID 271 285 BY SIMILARITY.
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 301 AA: 34907 MW; 3A29FIAFBA68FY298 CRC64;
 Query Match 19.6%; Score 251; DB 1; Length 301.
 Best Local Similarity 25.2%; Pred. No. 1.5e-14;
 Matches 65; Conservative 38; Mismatches 75; Indels 80; Gaps 7;
 42 FPKLCAALLIFELLAISFEIAFYI-----FFOKYS----- 73
 49 FPKRLCSTFRSLALAFNILLVICVSSQIQLEPRLKETFSNSSLMEFGA 108
 74 -----QLLEKTKELYHTLLECYKKNPV-----EETAMS 104
 109 LPTLGSTNAITLTMALQLEEKQADSHSTLFLHKLHPMDRLTLCOLAYFQNGTE 168
 105 CCPKMKSPSNCFISTESASWQSEKDCARMEHLVINOEDDFIIONQESAYF 164
 169 CCPVNVVERGSGSTWSSRDLTWAENDQICOLENALLVINSSEEDFYVKKH-RSOPHIM 227
 165 VGLSDEGGRHMQWQDTPYNESSTHREPSDPNRCVNLFRKSPKRG----- 216
 228 IGLTLDGGS--MKWVGTDRSNYRMMAFTQPD-----NMQHEGGGEGDCAEILS 276
 QY 217 ---WMDVNCGLPQRSYCE 231
 Db 277 DGHMNDNFCQVNRWVCE 294
 RESULT 2
 LECT_RAT
 ID LECT_RAT STANDARD; PRT; 301 AA.
 AC P08280;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1990 (Rel. 16, last sequence update)
 DE 30-MAY-2000 (Rel. 39, last annotation update)
 DE Asialoglycoprotein receptor R2/3 (Hepatic lectin 2/3) (RHL-2) (ASGP-R)
 DE (ASGP-R).
 GN ASGR2 OR ASGR-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87257885; PubMed=3600647;
 RA McPhaul M., Berg P.;
 RT Identification and characterization of cDNA clones encoding two
 RT homologous proteins that are part of the asialoglycoprotein
 RT receptor.";
 RL Mol. Cell. Biol. 7:1841-1847(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87250656; PubMed=3597443;
 RA Halberg D.F., Wager R.E., Farrell D.C., Hildreth J., Quesenberry M.S.,
 RA Loeb J.A., Holland E.C., Drickamer K.;
 RT Major and minor forms of the rat liver asialoglycoprotein receptor
 RT are independent galactose-binding proteins. Primary structure and
 RT glycosylation heterogeneity of minor receptor forms.";
 RL J. Biol. Chem. 263:9828-9838(1987).
 RN [3]

RP SEQUENCE FROM N.A.
 RX STRAIN=Sprague-Dawley; TISSUE=Liver;
 RC MEDLINE=89170119; PubMed=3234178;
 RA Sanford J.P., Elliott R.W., Doyle D.;
 RT "Asialoglycoprotein receptor genes are linked on chromosome 11 in the
 RT mouse.";
 RL DNA 7:721-728(1988).
 RN [4]
 RP SEQUENCE OF 201-301.
 RX MEDLINE=84111554; PubMed=6319386;
 RA Drickamer K., Mamon J.F., Bins G., Leung J.O.;
 RT "Primary structure of the rat liver asialoglycoprotein receptor.
 RT Structural evidence for multiple polypeptide species.";
 RL J. Biol. Chem. 259:770-778(1984).
 CC -1- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO
 CC WHICH THE TERMINAL SIALIC ACID RESIDE ON THEIR COMPLEX
 CC CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES
 CC TERMINAL GALACTOSE AND N-ACETYLGLACTOSAMINE UNITS. AFTER LIGAND
 CC BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AND
 CC TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE
 CC DISSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
 CC SURFACE.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN HEPATIC PARENCHYMAL
 CC CELLS.
 CC -1- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
 CC -1- MISCELLANEOUS: TWO TYPES OF RAT HEPATIC LECTIN HAVE BEEN
 CC IDENTIFIED, RHL-1 AND RHL-2/3, HAVING A RELATIVE ABUNDANCE OF 4:1.
 CC RHL-2 AND RHL-3 ONLY DIFFERS IN THEIR CARBOHYDRATE STRUCTURES.
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -----
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 CC -----
 CC EMBL: J16347; AAA42038.1; -
 CC EMBL: J02762; AAA41522.1; -
 CC EMBL: X07636; CAA30476.1; -
 CC PIR: B28462; LMR2.
 CC HSSP: P06734; IHLI.
 CC InterPro: IPR002353; AntifreezeII.
 CC InterPro: IPR001304; Lectin_C.
 CC InterPro: IPR005640; Lectin_N.
 CC Pfam: PF00059; Lectin_C.1.
 CC Pfam: PF03954; Lectin_N.1.
 CC PRINTS: PR00356; ANTIFREEZEII.
 CC SMART: SM00034; CLECT.1.
 CC DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
 DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
 KW Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
 KM Calcium; Signal-anchor; Phosphorylation.
 FT DOMAIN 1 58 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 59 79 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 80 301 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 169 295 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 170 181 BY SIMILARITY.
 FT DISULFID 198 285 BY SIMILARITY.
 FT DISULFID 271 293 BY SIMILARITY.
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 202 202 R -> A (IN REF. 1).
 FT CONFLICT 153 153 I -> N (IN REF. 2 AND 3).
 FT CONFLICT 202 202 C -> W (IN REF. 2 AND 3).
 FT CONFLICT 260 260
 SQ SEQUENCE 301 AA: 34943 MW; 3C2315B642D71279 CRC64;
 Query Match 18.1%; Score 232; DB 1; Length 301.
 Best Local Similarity 25.6%; Pred. No. 6.4e-13;

DE galactose/N-acetyl-galactosamine-specific lectin (MWGL).
 GN MGL1 OR MGL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=90293078; PubMed=2358462;
 RA I M., Kurata H., Itoh N., Yamashina I., Kawasaki T.;
 RT "Molecular cloning and sequence analysis of cDNA encoding the
 RT macrophage lectin specific for galactose and N-acetyl-galactosamine."
 RL J. Biol. Chem. 265:11295-11298(1990).
 RN [2]
 RP PRELIMINARY SEQUENCE OF 9-28.
 RX MEDLINE=88339956; PubMed=3421964;
 RA I M., Kawasaki T., Yamashina I.;
 RT "Structural similarity between the macrophage lectin specific for
 RT galactose/N-acetyl-galactosamine and the hepatic asialoglycoprotein
 RT binding protein."
 RL Biochem. Biophys. Res. Commun. 155:720-725(1988).
 CC -1- FUNCTION: RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE
 CC UNITS.
 CC -1- SUBUNIT: HOMO-OLIGOMER.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
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 CC EMBL: J05495; AAA41216.1; -
 CC PIR: A42230; A42230.
 DR HSSP: P06734; 1HLT.
 DR InterPro: IPR001304; Lectin_C.
 DR InterPro: IPR005640; Lectin_N.
 DR Pfam: PF00059; Lectin_C.1.
 DR Pfam: PF03954; Lectin_C.1.
 DR SMART: SM00034; CLECT.1.
 DR PROSITE: PS00615; C-TYPE_LLECTIN_1; 1.
 DR PROSITE: PS0041; C-TYPE_LLECTIN_2; 1.
 DR Lectin: Glycoprotein; Transmembrane; Calcium; Signal-anchor.
 KW DOMAIN 1
 KW TRANSMEM 38 57
 KW SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 KW (POTENTIAL).
 KW EXTRACELLULAR (POTENTIAL).
 KW C-TYPE LECTIN (LONG FORM).
 KW BY SIMILARITY.
 KW BY SIMILARITY.
 KW BY SIMILARITY.
 KW N-LINKED (GLCNAC...) (POTENTIAL).
 KW N-LINKED (GLCNAC...) (POTENTIAL).
 KW CARBOHYD 168 168
 KW CARBOHYD 34242 MW; D68A5DF0B9BF13 CRC64;
 SQ SEQUENCE 306 AA;
 Query Match 17.8%; Score 227.5; DB 1; Length 306;
 Best Local Similarity 31.6%; Pred. No. 1,6e-12;
 Matches 48; Conservative 27; Mismatches 62; Indels 15; Gaps 5;

RESULT 5
 LECH_CHICK
 ID LECH_CHICK STANDARD; PRT; 207 AA.
 AC P02707;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Hepatic lectin.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_Taxid=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91268022; PubMed=2050668;
 RA Bezouska K., Cichlow G.V., Rose J.M., Taylor M.E., Drickamer K.;
 RT "Evolutionary conservation of Intron position in a subfamily of genes
 RT encoding carbohydrate-recognition domains."
 RL J. Biol. Chem. 266:11604-11609(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88186849; PubMed=3281941;
 RA Mellow T.E., Halberg D., Drickamer K.;
 RT "Endocytosis of N-acetylglucosamine-containing glycoproteins by rat
 RT fibroblasts expressing a single species of chicken liver glycoprotein
 RT receptor."
 RL J. Biol. Chem. 263:5468-5473(1988).
 RN [3]
 RP SEQUENCE.
 RX MEDLINE=81215504; PubMed=7240175;
 RA Drickamer K.;
 RT "Complete amino acid sequence of a membrane receptor for
 RT glycoproteins. Sequence of the chicken hepatic lectin."
 RL J. Biol. Chem. 256:5827-5839(1981).
 CC -1- FUNCTION: HEPATIC LECTIN IS A MEMBRANE RECEPTOR PROTEIN THAT
 CC RECOGNIZES AND BINDS EXPOSED N-ACETYLGALACTOSAMINE MOIETIES OF
 CC PLASMA GLYCOPROTEINS, THUS MEDIATING THEIR CLEARANCE (FROM THE
 CC CIRCULATION) AND ENDOCYTOSIS.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- PTM: SOME OR ALL OF THE CYSTEINES ARE INVOLVED IN DISULFIDE BONDS.
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
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 CC EMBL: M63230; AAA48814.1; -
 CC EMBL: M63225; AAA48814.1; JOINED.
 CC EMBL: M63226; AAA48814.1; JOINED.
 CC EMBL: M63227; AAA48814.1; JOINED.
 CC EMBL: M63228; AAA48814.1; JOINED.
 CC EMBL: M63229; AAA48814.1; JOINED.
 CC EMBL: M63230; AAA48814.1; JOINED.
 CC PIR: J03188; AAA48937.1; -
 CC PIR: A03167; LNCNL.
 CC HSSP: P20693; 1HLT.
 CC InterPro: IPR001304; Lectin_C.
 CC Pfam: PF00059; Lectin_C.1.
 CC SMART: SM00034; CLECT.1.
 CC PROSITE: PS00615; C-TYPE_LLECTIN_1; 1.
 CC PROSITE: PS0041; C-TYPE_LLECTIN_2; 1.
 KW Lectin: Glycoprotein; Receptor; Endocytosis; Transmembrane;
 KW Signal-anchor; Acetylation.
 FT MOD_RES 1 1
 FT DOMAIN 1 23
 FT TRANSMEM 24 48
 FT ACETYLATION.
 FT CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT

[illegible]

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	CC	-----
DR	EMBL:	M10058; AAA51785.1; ..
DR	EMBL:	AB070933; BABB3508.1; ..
DR	PIR:	A22509; LNHUL.
DR	PDB:	1DV8; 26-JUL-00.
DR	Genew:	HGNC:742; ASGR1.
DR	MIM:	108360; ..
DR	GO:	GO:0004873; C:integral to plasma membrane; TAS.
DR	GO:	GO:0004873; F:asialoglycoprotein receptor activity; TAS.
DR	GO:	GO:0006898; P:receptor mediated endocytosis; TAS.
DR	InterPro:	IPR002353; AntifreezeII.
DR	InterPro:	IPR001304; Lectin_C.
DR	InterPro:	IPR005640; lectin_N.
DR	Pfam:	PF000059; lectin.C; 1.
DR	Pfam:	PF03954; lectin.N; 1.
DR	PRINTS:	PR00356; ANTIFREEZEII.
DR	SMART:	SM00034; CLECT; 1.
DR	PROSITE:	PS00615; C-TYPE_LECTIN_1; 1.
DR	PROSITE:	PS50041; C-TYPE_LECTIN_2; 1.
KW	Lectin:	Glycoprotein; Receptor; Endocytosis; Transmembrane; Calcium; Signal-anchor; Phosphorylation; 3D-structure.
FT	INIT_MET	0
FT	DOMAIN	1 39
FT	TRANSMEM	40 60
FT	DOMAIN	61 290
FT	SITE	4 7
FT	DISULFID	153 164
FT	DISULFID	181 276
FT	DISULFID	254 268
FT	CARBOHYD	80 80
FT	CARBOHYD	148 148
FT	SEQUENCE	290 AA; 33055 MW; B189/CE30DAE1586 CRC64;
Query Match		17.2%; Score 220.5; DB 1; Length 290;
Best Local Similarity		28.8%; Pred. No. 6e-12;
Matches	51; Conservative	28; Mismatches 75; Indels 23; Gaps 6;
OY	70 QKYSQLEKKTKTELVHT-----TLECVRKNMPEETAWSCCPNKMSSFSNCYFIS	121
DB	109 EKOKKDLSIEDHSLLTHVKOFVSDFLRSLSCOMALOCNGSERTCCPVNWWEHERSCYWS	168
OY	122 TESSMWDSKEDCARMEAHILVINTQEPDPIFNQLGEESAYFYGLSDPDEQRHWQVDQ	181
DB	169 RSGKAMADADNYCRLEDHNLVVATSWSEQRKFVQHIGGVNTW-MGLHDQNSP--WKWVDG	225
OY	182 TPYNESSTFWMPREPSD-----PNRCVVLNFRKSPKRGWMDVNCJGFORSVCE	231
DB	226 TDYELTGFRNMWRPEQPDDMYGHLGGEGDCA--HTDDGR---WNDDVCQGRRYRWYCE	277
RESULT 8		
LECH_MOUSE		
ID	LECH_MOUSE	STANDARD; PRT; 283 AA.
AC	P34927; O64363;	
DT	01-FEB-1994 (Rel. 28, Created)	
DT	15-JUL-1998 (Rel. 36, Last sequence update)	
DT	30-MAY-2000 (Rel. 39, Last annotation update)	
DE	Asialoglycoprotein receptor 1 (Hepatic lectin 1) (MH-1) (ASGP-R) (ASGPR).	
GN	ASGR1 OR ASGR-1.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	

```

RX MEDLINE=93176818; PubMed=8439656;
RA Takezawa R., Shinzawa K., Matanabe Y., Akaike T.;
RT "Determination of mouse major asialoglycoprotein receptor cDNA
   sequence.";
RL Biochim. Biophys. Acta 1172:220-222(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-Liver;
RA MEDLINE=95047431; PubMed=7958950;
RT Monroe R.S., Huber B.E.;
RL "The major form of the murine asialoglycoprotein receptor: cDNA
   sequence and expression in liver, testis and epididymis.";
RL Gene 148:237-244(1994).
CC -1- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO
   WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX
   CARBOHYDRATE MOETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES
   TERMINAL GALACTOSE AND N-ACETYLGLUCOSAMINE UNITS. AFTER LIGAND
   BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AND
   TRANSFERRED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE
   DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
   SURFACE.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN HEPATIC PARENCHYMAL
   CELLS.
CC -1- MISCELLANEOUS: CALCITONIN IS REQUIRED FOR LIGAND BINDING.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
CC EMBL: D13517; BAA02734.1; -
CC EMBL: U09362; AAB60441.1; -
CC EMBL: U08372; AAB60440.1; -
CC DR HSSP; P20693; 1HLJ.
CC DR MGD; MGI:88081; Asgpl.
CC DR InterPro: IPR002353; Antifreezeell.
CC DR InterPro: IPR001304; Lectin_C.
CC DR InterPro: IPR005640; Lectin_N.
CC DR Pfam; PF00059; Lectin_C.1.
CC DR Pfam; PF03954; Lectin_N.1.
CC DR PRINTS; PR00356; ANTIFREEZEELI.
CC DR SMART; SMO0034; CLECT.1.
CC DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
CC DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
CC DR Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
CC Calcium; Signal-anchor; Phosphorylation.
CC DR INIT MET 0 0
CC FT DOMAIN 1 38 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMM 39 59 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT (POTENTIAL).
CC FT DOMAIN 60 283 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 151 277 C-TYPE LECTIN (LONG FORM).
CC FT SITE 4 7 ENDOCYTOSIS SIGNAL (POTENTIAL).
CC FT DISULFD 152 163 BY SIMILARITY.
CC FT DISULFD 180 275 BY SIMILARITY.
CC FT DISULFD 253 267 BY SIMILARITY.
CC FT CARBOHYD 74 74 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC FT CARBOHYD 77 77 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC FT CARBOHYD 145 145 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC FT CONFLICT 150 150 I -> T (IN REF. 1).
CC SO SEQUENCE 283 AA; 32472 MW; 962A5D305AAED08F CXC64;

Query Match 17.0%; Score 218; DB 1; Length 283;
Best Local Similarity 27.7%; Pred. No. 9.6e-12;
Matches 51; Conservative 32; Mismatches 67; Indels 34; Gaps 7;

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Db      101 KLVSKELEKQCKDILEDHSSILLHLVKKOLSVSRSLSCOMAAFRNGSBERICCPINWVEYE    160
QY      115 SNCFYFISTESASWODESKDCARMEAHLLVTINTOEODFIQNLQEEASYFVGISDPGQR    174
       111:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      161 GSCYWFSSSYRPFMTADKYCCOLENAHLVVVTSRDENFLORHMGPLNTM--IGLTDQNGP    218
QY      175 HMCWAVDDPTYNESSTFWHPRPSD-----PNRCYVLNFRKSPKRMGNVDVCGLPQR    227
       111:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      219 -WKWVSDGTIDYETGFQNRRPDQNMWYGHGLEGEDCA--HFTLDGR--WNDDVCRRPYR    272
OY      228 SVCE    231
       |||
Db      273 WVCE    276

RESULT 9
MMGL_MOUSE
ID      MMGL_MOUSE          STANDARD;          PRT;          304 AA.
AC      P49300.
DT      01-FEB-1996 (Rel. 33, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Macrophage asialoglycoprotein-binding protein 1 (M-ASGP-BP)
DN      (Macrophage galactose/N-acetylgalactosamine specific lectin) (MMGL).
GN      MG1 OR MGL.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      NCBI_TaxId=10090;
[1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C3H/HEN;
RX      MEDLINE=92268032; PubMed=1587794;
RA      Sato M., Kawakami K., Osawa T., Toyoshima S.;
RT      "Molecular cloning and expression of cDNA encoding a galactose/N-
RL      acetyl-galactosamine-specific lectin on mouse tumoricidal
RN      macrophages."
RL      J. Biochem. 111:331-336(1992).
[2]
RP      SEQUENCE OF 102-120 AND 137-151.
RC      STRAIN=C3H/HEN;
RX      MEDLINE=89197865; PubMed=3241002;
RA      Oda S., Sato M., Toyoshima S., Osawa T.;
RT      "Purification and characterization of a lectin-like molecule specific
RL      for galactose-N-acetyl-galactosamine from tumoricidal macrophages.";
RJ      J. Biochem. 104:600-605(1988).
-|- FUNCTION: RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE
UNIT(S). MAY PARTICIPATE IN THE INTERACTION BETWEEN TUMORICIDAL
MACROPHAGES AND TUMOR CELLS.
-|- SUBUNIT: MONO-OLIGOMER.
-|- SUBCELLULAR LOCATION: Type II membrane protein.
-|- TISSUE SPECIFICITY: IS EXPRESSED ON THE SURFACE OF ACTIVATED
MACROPHAGES.
-|- SIMILARITY: Contains 1 C-type lectin family domain.
-----
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CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL: S36576; AAB22171.1; -.
DR      PIR: JX0209; JX0209.
DR      HSSP: P06734; IHLI.
DR      MGD: MGI:96975; Mg1l.
DR      InterPro: IPR002353; Antifreeze1l.
DR      InterPro: IPR001304; Lectin_C.
DR      InterPro: IPR005640; Lectin_N.
DR      Pfam: PF00059; Lectin_C_1.
DR      Pfam: PF03954; Lectin_N_1.
DR      PRINTS: PR00356; ANTIFREEZE1L.

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DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN.1; 1.
 DR PROSITE; PS00411; C-TYPE LECTIN.2; 1.
 KW Lectin; Glycoprotein; Transmembrane; Calcium; Signal-anchor.
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 57 304 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 172 298 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 173 184 BY SIMILARITY.
 FT DISULFID 201 296 BY SIMILARITY.
 FT CARBOHYD 274 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 304 AA; 34596 MW; 3F79CD12C34F5BCC CRC64;
 Query Match 16.9%; Score 216.5; DB 1; Length 304;
 Best Local Similarity 31.1%; Pred. No. 1.4e-11;
 Matches 47; Conservative 25; Mismatches 64; Indels 15; Gaps 5;
 89 LECVKNMPEETAWSCCPKMKSFSSNCFISTESAWQDSEKDCARMEAHLLVINTOE 148
 156 LFCQLANLNKNGSEVACPLHWTHEGSCYWFSESKSPKADKRYLNSHLVYVNSLE 215
 149 EDDFETQNLQESATFVGLSDPEGORHMQWVDQTPYNESSTWHPREPSD-----PNE 201
 216 EGNFL-QNRLANVVSIGLIDONGP--WRWVDGTDEKGFKNWAPLQPDNMGHGLGGE 272
 202 RCVLNFRKSPKRWGMDVNCIGPORSVCEM 232
 273 DCAHIT-TGGP-----WDDVCOPTFRWICEM 298
 Db
 QY 202 RCVLNFRKSPKRWGMDVNCIGPORSVCEM 232
 Db 273 DCAHIT-TGGP-----WDDVCOPTFRWICEM 298
 Db
 RESULT 10
 KUCR.MOUSE
 ID KUCR.MOUSE STANDARD; PRT; 548 AA.
 AC P70194;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-type lectin 13 (Kupffer cell receptor).
 GN CLEC5F13 OR KCLR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN-BALB/c; TISSUE-Liver;
 RA Takezawa R., Magatsuma H., Nomoto C., Watanabe Y., Akaike T.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: RECEPTOR WITH AN AFFINITY FOR GALACTOSE AND FUCOSE.
 CC COULD BE INVOLVED IN ENDOCYTOSIS.
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -I- TISSUE SPECIFICITY: KUPFFER CELLS.
 CC -I- SIMILARITY: Contains 1 C-type lectin family domain.
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 CC -----
 DR EMBL; D88577; BAA13647.1; -
 DR HSSP; P20693; 1HLT;
 DR MGD; MGI:1859634; Clec5f13.
 DR InterPro; IPR002353; AntifreezeII.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR PRINTS; PR00356; ANTIFREEZEII.
 DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS00615; C-TYPE LECTIN.1; 1.
 DR PROSITE; PS00411; C-TYPE LECTIN.2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Lectin; signal-anchor;
 FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 43 69 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 70 548 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 438 538 C-TYPE LECTIN (SHORT FORM).
 FT DISULFID 440 536 BY SIMILARITY.
 FT DISULFID 516 528 BY SIMILARITY.
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 548 AA; 61268 MW; 6F6495E820E73BD9 CRC64;
 Query Match 16.6%; Score 213; DB 1; Length 548;
 Best Local Similarity 30.6%; Pred. No. 5.5e-11;
 Matches 45; Conservative 25; Mismatches 61; Indels 16; Gaps 4;
 93 KKNMPEETAWSCCPKMKSFSSNCFISTESAWQDSEKDCARMEAHLLVINTOEQDF 152
 399 KOEQKTONOVLOLIDMQMKRYFNENFYFSDRKPMKEAKFCTSGCAHLASVTSOEEQAF 458
 153 IFQNLQESATFVGLSDPEGORHMQWVDQTPYN--ESSFWHPREPSD-----PNERCV 204
 459 LVQV-TSSDDHWIGLIDQGTBGIWRVVDTPPPNMAOSKGFQWKNQPDNRHNGEREDCV 517
 205 VLNFRKSPKRWGMDVNCIGPORSVCE 231
 518 HV-----RQQMDMACGSSYPWCK 537
 Db
 QY 205 VLNFRKSPKRWGMDVNCIGPORSVCE 231
 Db 518 HV-----RQQMDMACGSSYPWCK 537
 Db
 RESULT 11
 FCER2.MOUSE
 ID FCER2.MOUSE STANDARD; PRT; 331 AA.
 AC P20693; Q61556; Q61557;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Low affinity immunoglobulin epsilon FC receptor (Lymphocyte IGE
 DE receptor) (FC-epsilon-RI) (CD23).
 GN FCER2 OR FCER2A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 [1]
 SEQUENCE FROM N.A.
 RX MEDLINE-90017519; PubMed-2529542;
 RA Bettler B., Hofstetter H., Rao M., Yokoyama W.M., Kilcherr F.,
 RT "Molecular structure and expression of the murine lymphocyte low-
 RT affinity receptor for IGE (Fc epsilon RI)".
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7566-7570(1989).
 [2]
 SEQUENCE FROM N.A.
 RX MEDLINE-90171598; PubMed-2137845;
 RA Gollnick S.O., Trounstein M.L., Yamashita L.C., Kehry M.R.,
 RA Moore K.W.;
 RT "Isolation, characterization, and expression of cDNA clones encoding
 RT the mouse Fc receptor for IGE (Fc epsilon RI)1.";
 RL J. Immunol. 144:1974-1982(1990).
 [3]
 SEQUENCE FROM N.A. (ISOFORMS B AND C).
 RC STRAIN-DBA/2;
 RX MEDLINE-94372613; PubMed-8086828;
 RA Kondo H., Ichikawa Y., Nakamura K., Tsuchiya S.;
 RT "Cloning of cDNAs for new subtypes of murine low-affinity Fc receptor
 RT for Ige (Fc epsilon RI/CD23).";

RL Int. Arch. Allergy Immunol. 105:38-48(1994).
 RN [4]
 RP 3D-STRUCTURE MODELING OF LECTIN DOMAIN.
 RX MEDLINE=94191542; PubMed=8142907;
 RA Padian E.A., Helm B.A.;
 RT "Modeling of the lectin-homology domains of the human and murine low-
 affinity Fc epsilon receptor (Fc epsilon RI/CD23)."
 RL Receptor 3:325-341(1993).
 CC -1- FUNCTION: THIS RECEPTOR HAS ESSENTIAL ROLES IN THE REGULATION OF
 CC ICE PRODUCTION AND IN THE DIFFERENTIATION OF B-CELLS (IT IS A B-
 CC CELL-SPECIFIC ANTIGEN).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-3;
 CC Name-A:
 CC IsoId=P20693-1; Sequence=Displayed;
 CC Name-B:
 CC IsoId=P20693-2; Sequence=VSP_003058;
 CC Name-C:
 CC IsoId=P20693-3; Sequence=VSP_003059;
 CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
 CC -1- MISCELLANEOUS: THERE ARE TWO KINDS OF FC RECEPTORS FOR ICE, WHICH
 CC DIFFER IN BOTH STRUCTURE AND FUNCTION: HIGH AFFINITY RECEPTORS ON
 CC BASOPHILS AND MAST CELLS AND LOW AFFINITY RECEPTORS ON LYMPHOCYTES
 CC AND MONOCYTES.
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -----
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 CC -----
 DR EMBL: M99371; AAA74898.1; -
 DR EMBL: M34163; AAA37603.1; -
 DR EMBL: X64223; CAA45532.1; -
 DR EMBL: X64224; CAA45533.1; -
 DR PIR: A43518; LNMSE.
 DR PDB: 1HLI; 3I-JAN-94.
 DR MGD: MGI:95497; Fcgr2a.
 DR InterPro: IPR002353; Antifreeze1.
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam: PF00059; lectin_c.1.
 DR PRINTS: PR00356; ANTIREEZE1.
 DR SMART: SM00034; CLECT.1.
 DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
 DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
 DR Repeat: Lectin; Signal-anchor; Glycoprotein; Receptor; B-cell;
 DR Repeat: Lectin; Signal-anchor; Alternative splicing; 3D-structure.
 DR DOMAIN 1 23
 DR TRANSEM 24 49
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT C-TYPE LECTIN (LONG FORM).
 FT
 FT DOMAIN 50 331
 FT DOMAIN 185 298
 FT REPEAT 71 91
 FT REPEAT 92 112
 FT REPEAT 113 133
 FT DISULFID 183 311
 FT DISULFID 186 197
 FT DISULFID 214 305
 FT DISULFID 282 296
 FT CARBOHYD 65 65
 FT CARBOHYD 114 114
 FT VARSPLIC 1 7
 FT VARSPLIC 1 7
 FT STRAND 197 200
 FT HELIX 207 216
 FT TURN 217 218
 FT STRAND 220 221

FT HELIX 227 237
 FT TURN 238 239
 FT STRAND 242 247
 FT TURN 249 250
 FT TURN 252 253
 FT STRAND 256 257
 FT TURN 258 259
 FT STRAND 260 262
 FT STRAND 268 268
 FT TURN 270 271
 FT TURN 277 278
 FT STRAND 282 285
 FT TURN 287 288
 FT STRAND 291 294
 FT TURN 296 297
 FT STRAND 304 307
 SQ SEQUENCE 331 AA; 37647 MW; B8C6D65F34ACDB2 CRC64;
 Query Match 16.3%; Score 208.5; DB 1; Length 331;
 Best Local Similarity 31.2%; Pred. No. 7.6e-11;
 Matches 53; Conservative 34; Mismatches 60; Indels 23; Gaps 8;
 QY 75 LLEKRTKELVHTTLECVK---NMPVETAMSCPRKMKSFSSNCFITSTESASMODS 130
 DB 151 LNEKRTASDSLEKIQEFAKIMIEILISKYACNICPKNMLHFQOKCYFGKSGKQWIA 210
 QY 131 EKDCARMEAHILVINTQEDDFIQNLQESAYVGLSDPGRQRMQVQTPYNESSTF 190
 DB 211 RFACSDIAGRLVSHSOKEDFLMQHINKKDSW-IGLQDLNMEGEFWSGSPVGSN-- 267
 QY 191 WHPREPSD--PNERCVLNFRRKSPKRMGMDVNCIGPORS----VCEMM 233
 DB 268 WNEPEPNNGGGEGDCVMM--RGSQ---WMDAFC----RSLDAMVCEQL 308
 RESULT 12
 KUCR_RAT
 ID KUCR_RAT STANDARD; PRT; 550 AA.
 AC P10716;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-type lectin 13 (Kupffer cell receptor).
 GN CLEC5F13 OR KCLR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 83-104.
 RX MEDLINE=88227939; PubMed=2836387;
 RA Hoyle G.W., Hill R.L.;
 RT "Molecular cloning and sequencing of a cDNA for a carbohydrate
 RT binding receptor unique to rat Kupffer cells."
 RL J. Biol. Chem. 263:7487-7492(1988).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91107689; PubMed=1846367;
 RA Hoyle G.W., Hill R.L.;
 RT "Structure of the gene for a carbohydrate-binding receptor unique to
 RT rat Kupffer cells."
 RL J. Biol. Chem. 266:1850-1857(1991).
 CC -1- FUNCTION: RECEPTOR WITH AN AFFINITY FOR GALACTOSE AND FUCOSE.
 CC COULD BE INVOLVED IN ENDOCYTOSIS.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- TISSUE SPECIFICITY: KUPFFER CELLS.
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -----
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CC DR EMBL: J03734; AAA41472.1; -

CC DR EMBL: M55533; AAA40892.1; -

DR PIR: A38674; A28166.

DR HSSP: P20693; 1HLJ.

DR InterPro: IPR002353; AntifreezeII.

DR InterPro: IPR001304; Lectin_C.

DR Pfam: PF00059; Lectin_C.1.

DR PRINTS: PR00356; ANTIFREEZEII.

DR SMART: SM00034; CLECT.1.

DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.

DR PROSITE: PS0041; C-TYPE_LECTIN_2; 1.

KW Receptor; Transmembrane; Glycoprotein; Lectin; Signal-anchor; Endocytosis.

FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 43 69 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).

FT DOMAIN 70 550 EXTRACELLULAR (POTENTIAL).

FT DISULFID 438 538 C-TYPE LECTIN (SHORT FORM).

FT DISULFID 516 528 BY SIMILARITY.

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SQUENCE 550 AA; 61104 MW; 9358A6CF4C306270 CRC4;

Query Match 15.38; Score 196; DB 1; Length 550;
-best Local Similarity 31.88; Pred. No. 1.6e-09;
Matches 42; Conservative 23; Mismatches 51; Indels 16; Gaps 4;

QY 108 KMKKSSNCYFTSTSSASMODEKCAKMEALVYINQEDDFPQNIQESAFVGL 167
DB 414 QMKRYNGKRYFSRKSKMHEANFCVSGALASVTSQEEAFVQ-ITNAVDMWIGL 472
QY 168 SPEGQRHQQWVDQF--YNESSTFWHPREPSD-----PNERCVYLNFRKSPRWGMW 219
DB 473 TDGGTGNRWVDGTFEDVQSRFRKQGPDMWRNGNREDCVHLQRM-----WMD 525
QY 220 VNCIGPQRSVCE 231
DB 526 MACGTAYNMWCK 537

RESULT 13
PCGN_MOUSE STANDARD; PRT; 1268 AA.

AC P55066;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neutocan core protein precursor (Chondroitin sulfate proteoglycan 3).
GN Cspg3 OR NCAN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-Brain;
RX MEDLINE=96039250; PubMed=7490074;
RA Rauch U., Grilme B., Kulbe G., Arnold-Ammer I., Beler D., Faessler R.;
RT "Structure and chromosomal localization of the mouse neutocan gene";
RL Genomics 28:405-410(1995).
CC -i- FUNCTION: May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NC-CAM and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic acid.

CC -i- TISSUE SPECIFICITY: BRAIN.

CC -i- SIMILARITY: Contains 1 Immunoglobulin-like V-type domain.

CC -i- SIMILARITY: Contains 2 EGF-like domains.

CC -i- SIMILARITY: Contains 2 link domains.

CC -i- SIMILARITY: Contains 1 C-type lectin family domain.

CC -i- SIMILARITY: Contains 1 Sushi (SCR) domain.

CC -i- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.

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CC EMBL: X64727; CA59216.1; -

DR PIR: S52781; S52781.

DR HSSP: P00740; 1EDM.

DR MGD: MGI:104694; Cspg3.

DR InterPro: IPR002353; AntifreezeII.

DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR000742; EGF-2.

DR InterPro: IPR001861; EGF_Ca.

DR InterPro: IPR006209; EGF_Like.

DR InterPro: IPR007110; Ig_Like.

DR InterPro: IPR003599; Ig.

DR InterPro: IPR003306; Ig_MHC.

DR InterPro: IPR001304; Lectin_C.

DR InterPro: IPR000338; Link.

DR InterPro: IPR000436; Sushi_SCR_CCP.

DR Pfam: PF00008; EGF; 2.

DR Pfam: PF00047; Ig; 1.

DR Pfam: PF00059; Lectin_C; 1.

DR Pfam: PF00084; sushi; 1.

DR Pfam: PF00193; Xlink; 2.

DR PRINTS: PR01265; LINKMODULE.

DR PRINTS: PR00356; ANTIFREEZEII.

DR PRODOM: PD000918; Link; 2.

DR SMART: SM00032; CCP; 1.

DR SMART: SM00034; CLECT; 1.

DR SMART: SM00179; EGF_CA; 1.

DR SMART: SM00409; IG; 1.

DR SMART: SM00445; LINK; 2.

DR PROSITE: PS00010; ASX_HYDROXYL; 1.

DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.

DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.

DR PROSITE: PS00022; EGF_1; 3.

DR PROSITE: PS01186; EGF_2; 1.

DR PROSITE: PS01187; EGF_CA; 1.

DR PROSITE: PS50835; IG_Like; 1.

DR PROSITE: PS01241; LINK; 2.

KW Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 1268 NEUROCAN CORE PROTEIN.

FT DOMAIN 37 157 IG-LIKE V-TYPE.

FT DOMAIN 158 253 LINK 1.

FT DOMAIN 259 355 LINK 2.

FT DOMAIN 960 996 EGF-LIKE 1.

FT DOMAIN 998 1034 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 1036 1165 C-TYPE LECTIN.

FT DOMAIN 1166 1224 SUSHI.

FT DISULFID 58 139 BY SIMILARITY.

FT DISULFID 181 252 BY SIMILARITY.

FT DISULFID 205 226 BY SIMILARITY.

FT DISULFID 279 354 BY SIMILARITY.

FT DISULFID 303 324 BY SIMILARITY.

FT DISULFID 964 975 BY SIMILARITY.

FT DISULFID 969 984 BY SIMILARITY.

FT DISULFID 986 995 BY SIMILARITY.

FT DISULFID 1040 1051 BY SIMILARITY.

FT DISULFID 1068 1160 BY SIMILARITY.

FT CARBOHYD 1164 1164 N-LINKED (GLCNAC..) (POTENTIAL).
SQ SEQUENCE 1257 AA; 135544 MW; 992B33DCFA19EE1B CRC64;
Query Match 14.4%; Score 184; DB 1; Length 1257;
Best Local Similarity 31.7%; Pred. No. 4.5e-08;
Matches 38; Conservative 22; Mismatches 50; Indels 10; Gaps 4;
QY 106 CPKMKSFSSNCYFISTESASWDSKDCARMEAHLLVINTOEODPIFONLOESAYFV 165
DB 1029 CDRGWHKFGCHCYRYFAHRRAMEDAEKDCRRRAGHLTSVSPBEHFFINSFGHENS--WI 1086
QY 166 GLSDPEGRHMQWVDOTPYNESSTFWHPREPSD---PNEKCVLNRKSPKRGWMDVNC 222
DB 1087 GLNDRIVERDFQWTDNTGLQYEN--WRKOPDNFFAGGEDCVYVAHENGMR---WMDVPC 1141
RESULT 15
PGCN_HUMAN STANDARD; PRT; 1321 AA.
014594; Q90PK6;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3).
GN CSPG3 OR NCAN OR NEUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=99013874; PubMed=9795216;
RT Prange C.K., Pennacchio L.A., Hleuallen K., Fan W., Lennon G.G.;
RL "Characterization of the human neurocan gene, CSPG3.";
RL Gene 221:199-205(1998).
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Gaines J.,
Dangnan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
Liu S., Altix C., Andreise T., Trankheim M., Amico-Keller G.,
Coeffield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
Kobayashi A., Olsen A.S., Carrano A.V.;
RA "Sequence analysis of an ~1 Mb region containing the MEF2B gene in
19p12.";
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May modulate neuronal adhesion and neurite growth during
development by binding to neural cell adhesion molecules (NG-CAM
and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronate
acid.
CC -!- TISSUE SPECIFICITY: Brain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 2 link domains.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF026547; AAC80576.1; -
DR EMBL; AC006310; AAB86655.1; -
DR EMBL; AC005254; AAC25581.1; -
DR HSSP; P00740; 1EDM
DR Genew; HGNC:2465; CSPG3.

DR MIM; 600826; -
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR000538; Link.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00059; lectin_C; 1.
DR Pfam: PF00084; sushi; 1.
DR Pfam: PF00193; Xlink; 2.
DR PRINTS: PR01265; LINKMODULE.
DR PRODOM: PD000918; Link; 2.
DR SMART: SM00032; CCP; 1.
DR SMART: SM00034; CLECT; 1.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00445; LINK; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
DR PROSITE: PS00022; EGF_1; 3.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00835; IGLIKE; 1.
DR PROSITE: PS01241; LINK; 2.
KW Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
KW EGF-like domain; Calcium; Repeat; Sushi; signal.
FT SIGNAL 1 22
FT CHAIN 23 1321
FT DOMAIN 38 153
FT DOMAIN 159 254
FT DOMAIN 260 356
FT DOMAIN 1008 1044
FT DOMAIN 1046 1082
FT DOMAIN 1084 1213
FT DOMAIN 1214 1272
FT DISULFID 59 140
FT DISULFID 182 253
FT DISULFID 206 227
FT DISULFID 280 355
FT DISULFID 304 325
FT DISULFID 1012 1023
FT DISULFID 1017 1032
FT DISULFID 1034 1043
FT DISULFID 1088 1099
FT DISULFID 1116 1208
FT DISULFID 1184 1200
FT DISULFID 1215 1258
FT DISULFID 1244 1271
FT CARBOHYD 122 122
FT CARBOHYD 340 340
FT CARBOHYD 1026 1026
FT CARBOHYD 1223 1223
FT CARBOHYD 1234 1234
FT CONFLICT 1254 1254
FT CONFLICT 1282 1282
SQ SEQUENCE 1321 AA; 142972 MW; 2EF4F823DB980B8 CRC64;
Query Match 14.4%; Score 184; DB 1; Length 1321;
Best Local Similarity 32.5%; Pred. No. 4.8e-08;
Matches 39; Conservative 20; Mismatches 51; Indels 10; Gaps 4;
QY 106 CPKMKSFSSNCYFISTESASWDSKDCARMEAHLLVINTOEODPIFONLOESAYFV 165
DB 1088 CDRGWHKFGCHCYRYFAHRRAMEDAEKDCRRRAGHLTSVSPBEHFFINSFGHENT--WI 1145
QY 166 GLSDPEGRHMQWVDOTPYNESSTFWHPREPSD---PNEKCVLNRKSPKRGWMDVNC 222

Db 1146 GLNDRIVERDFOWTDNGLQFEN--WRNQPDNFFAGGEDCVVVAHESGR---WMDVPC 1200

Search completed: August 4, 2003, 13:09:09
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 13:05:28 ; Search time 96 Seconds
(without alignments)
637.067 Million cell updates/sec

Title: US-09-862-802-2
Perfect score: 1280
Sequence: 1 MTSEITVAEVRFKNEFKSSG.....NDVNCLEPQSRVCEMMKIH 237

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	1280	100.0	237 4 Q9UI34	Q9UI34 homo sapien
2	1275	99.6	237 4 Q9NS33	Q9NS33 homo sapien
3	1273	99.5	237 4 Q9UMR7	Q9UMR7 homo sapien
4	1231	96.2	230 4 Q8WXR9	Q8WXR9 homo sapien
5	1079.5	84.3	204 4 Q9H229	Q9H229 homo sapien
6	672.5	52.5	238 11 Q9GZ15	Q9GZ15 mus musculu
7	650.5	50.8	262 11 Q923C7	Q923C7 mus musculu
8	551.5	43.1	213 4 Q8WTR0	Q8WTR0 homo sapien
9	533.5	41.7	182 4 Q8WXR8	Q8WXR8 homo sapien
10	489	38.2	209 11 Q9JRF4	Q9JRF4 mus musculu
11	476.5	37.2	158 11 Q8JZX6	Q8JZX6 mus musculu
12	452.5	35.4	175 11 Q9JRF3	Q9JRF3 mus musculu
13	447	34.9	176 11 Q9D8Q7	Q9D8Q7 mus musculu
14	440.5	34.4	152 11 Q8CIG3	Q8CIG3 mus musculu
15	400	31.2	215 4 Q8NS55	Q8NS55 homo sapien
16	399	31.2	215 4 Q8WXR8	Q8WXR8 homo sapien

17	352.5	27.5	219 11 Q922H6	Q922H6 mus musculu
18	352.5	27.5	219 11 Q8C212	Q8C212 mus musculu
19	330.5	25.8	168 11 Q9JRF2	Q9JRF2 mus musculu
20	330	25.8	219 4 Q9ULY5	Q9ULY5 homo sapien
21	325.5	25.4	214 11 Q9R0Q8	Q9R0Q8 mus musculu
22	256.5	20.0	292 4 Q14538	Q14538 homo sapien
23	253.5	19.8	236 13 Q8U0M9	Q8U0M9 oryzias lat
24	253	19.8	316 4 Q8IUN9	Q8IUN9 homo sapien
25	243	19.0	208 11 Q912W7	Q912W7 mus musculu
26	233	18.2	237 11 Q912W8	Q912W8 mus musculu
27	232	18.1	263 4 Q96QP3	Q96QP3 homo sapien
28	232	18.1	376 4 Q9BXS3	Q9BXS3 homo sapien
29	232	18.1	399 4 Q9H2X3	Q9H2X3 homo sapien
30	230.5	18.0	332 4 Q96QP5	Q96QP5 homo sapien
31	230	18.0	256 6 Q8MIS5	Q8MIS5 macaca mula
32	230	18.0	399 6 Q8HY12	Q8HY12 hylobates l
33	230	18.0	399 6 Q8HY10	Q8HY10 hylobates c
34	226	17.7	422 6 Q8HY11	Q8HY11 hylobates s
35	225	17.6	381 6 Q8HY02	Q8HY02 hylobates s
36	224	17.5	445 6 Q8HY05	Q8HY05 pan troglod
37	223	17.4	238 11 Q912X1	Q912X1 mus musculu
38	223	17.4	376 6 Q8HY06	Q8HY06 gorilla gor
39	223	17.4	445 6 Q8HYC0	Q8HYC0 pan troglod
40	221	17.3	284 11 Q91Y84	Q91Y84 mus musculu
41	221	17.3	399 4 Q9H2Q9	Q9H2Q9 homo sapien
42	219.5	17.1	322 11 Q8CJ89	Q8CJ89 mus musculu
43	219.5	17.1	742 4 Q9BYH7	Q9BYH7 homo sapien
44	217.5	17.0	417 4 Q8TCR2	Q8TCR2 homo sapien
45	217.5	17.0	742 4 Q8WZA4	Q8WZA4 homo sapien

ALIGNMENTS

RESULT 1	
Q9UI34	
AC Q9UI34:	PRELIMINARY; PRT; 237 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)	
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DE C-type lectin superfamily 6.	
GN CLCSPF.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Richard M., Beaulieu A.D.;	
RT "A novel C-type lectin expressed in GM-CSF stimulated neutrophils."	
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AF109146; AAF14348.1; -	
DR InterPro; IPR001304; Lectin_C.	
DR Pfam; PF00059; Lectin_C; 1.	
DR SMART; SM00034; CLECT; 1.	
DR PROSITE; PS00615; C-TYPE_LLECTIN_1; 1.	
DR PROSITE; PS50041; C-TYPE_LLECTIN_2; 1.	
KW Lectin.	
SO SEQUENCE 237 AA; 27488 MW; 1A68BCE8323345BA CRC64;	
Query Match	100.0%; Score 1280; DB 4; Length 237;
Best Local Similarity	100.0%; Pred. No. 8.2e-117;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 MTSEITVAEVRFKNEFKSSGINTASSASKERTAPLKSNTGFPKLLCASLLIFLLLAIS 60	
DB 1 MTSEITVAEVRFKNEFKSSGINTASSASKERTAPLKSNTGFPKLLCASLLIFLLLAIS 60	
QY 61 FFIAFVIFPQKYSQLEKTKTKELVHTTLECVKKNMPVEETFAWSCCPKNMKSFSNCYFI 120	
DB 61 FFIAFVIFPQKYSQLEKTKTKELVHTTLECVKKNMPVEETFAWSCCPKNMKSFSNCYFI 120	


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OY 121 STESASWQDSEKDCARMEAHLLVINTQEDDFITQNOESATFVGLSDPEGGRHQMWD 180
DB 121 STESASWQDSEKDCARMEAHLLVINTQEDDFITQNOESATFVGLSDPEGGRHQMWD 180
OY 181 QTPYNESSTFWHREPSPDNERCVLVNFRKSPKRMGMNDVNCGLGPORSVCEMMKIH 237
DB 181 QTPYNESSTFWHREPSPDNERCVLVNFRKSPKRMGMNDVNCGLGPORSVCEMMKIH 237

RESULT 2
O9NS33 PRELIMINARY; PRT; 237 AA.
ID 09NS33
AC 09NS33
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE H0CGC13P.
OS Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A.
RA Zhao Z., Huang X., Li N., Zhu X., Cao X.;
RT "Novel gene identified from dendritic cells."
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF067800; AAF75560.1;
DR Genew; HGNC:13257; CLECSF6.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
SQ SEQUENCE 237 AA; 27504 MW; 71197BFD337651EB CRC64;

Query Match 99.6%; Score 1275; DB 4; Length 237;
Best Local Similarity 99.6%; Pred. No. 2.5e-116;
Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MISEITVAEVRKNEFKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFFLLAIS 60
DB 1 MISEITVAEVRKNEFKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFFLLAIS 60
OY 61 FFLAFAVIFPKYSOLLEKTKTKELVHTTLECVKKNMPVEETAMSCCPKMKSSSNCYFI 120
DB 61 FFLAFAVIFPKYSOLLEKTKTKELVHTTLECVKKNMPVEETAMSCCPKMKSSSNCYFI 120
DB 121 STESASWQDSEKDCARMEAHLLVINTQEDDFITQNOESATFVGLSDPEGGRHQMWD 180
DB 121 STESASWQDSEKDCARMEAHLLVINTQEDDFITQNOESATFVGLSDPEGGRHQMWD 180
OY 181 QTPYNESSTFWHREPSPDNERCVLVNFRKSPKRMGMNDVNCGLGPORSVCEMMKIH 237
DB 181 QTPYNESSTFWHREPSPDNERCVLVNFRKSPKRMGMNDVNCGLGPORSVCEMMKIH 237

RESULT 3
O9UMR7 PRELIMINARY; PRT; 237 AA.
ID 09UMR7
AC 09UMR7
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Dendritic cell immunoreceptor.
OS Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A.
RA MEDLINE=93370001; Pubmed=10438934;
RX Bates E.E., Fournier N., Garcia E., Valladeau J., Durand I., Pin J.T.,

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RA Zurawski S.M., Patel S., Abrams J.S., Lebecque S., Garrone P.,
RA Saeland S.;
RT "APCs express DCIR, a novel c-type lectin surface receptor containing
RT an immunoreceptor tyrosine-based inhibitory motif."
RL J. Immunol. 163:1973-1983(1999).
DR EMBL: AJ133532; CAB54001.1;
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 237 AA; 27512 MW; 1D07003E4C9C9F6E CRC64;

Query Match 99.5%; Score 1273; DB 4; Length 237;
Best Local Similarity 99.6%; Pred. No. 3.9e-116;
Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MISEITVAEVRKNEFKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFFLLAIS 60
DB 1 MISEITVAEVRKNEFKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFFLLAIS 60
OY 61 FFLAFAVIFPKYSOLLEKTKTKELVHTTLECVKKNMPVEETAMSCCPKMKSSSNCYFI 120
DB 61 FFLAFAVIFPKYSOLLEKTKTKELVHTTLECVKKNMPVEETAMSCCPKMKSSSNCYFI 120
DB 121 STESASWQDSEKDCARMEAHLLVINTQEDDFITQNOESATFVGLSDPEGGRHQMWD 180
DB 121 STESASWQDSEKDCARMEAHLLVINTQEDDFITQNOESATFVGLSDPEGGRHQMWD 180
OY 181 QTPYNESSTFWHREPSPDNERCVLVNFRKSPKRMGMNDVNCGLGPORSVCEMMKIH 237
DB 181 QTPYNESSTFWHREPSPDNERCVLVNFRKSPKRMGMNDVNCGLGPORSVCEMMKIH 237

RESULT 4
O8XW9 PRELIMINARY; PRT; 230 AA.
ID 08XW9
AC 08XW9
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Fc-epsilon receptor III.
OS Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A.
RA Zhang W., Zhang J., Li N., Wan T., Chen T., Cao X.;
RT "Novel human Fc-epsilon receptor III."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF328684; AAL56016.1;
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 230 AA; 26603 MW; 03CAB867D71BB084 CRC64;

Query Match 96.2%; Score 1231; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.8e-112;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MISEITVAEVRKNEFKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFFLLAIS 60
DB 1 MISEITVAEVRKNEFKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFFLLAIS 60
OY 61 FFLAFAVIFPKYSOLLEKTKTKELVHTTLECVKKNMPVEETAMSCCPKMKSSSNCYFI 120
DB 61 FFLAFAVIFPKYSOLLEKTKTKELVHTTLECVKKNMPVEETAMSCCPKMKSSSNCYFI 120

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QY 121 STESASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORHOMWD 180
DB 121 STESASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORHOMWD 180
QY 181 QTPYNESSTFWHPRPSDPNERCVLNFRRKSPKRGWMDVNCIGPQRS 228
DB 181 QTPYNESSTFWHPRPSDPNERCVLNFRRKSPKRGWMDVNCIGPQRS 228

RESULT 5

Q9H229 PRELIMINARY: PRT: 204 AA.
AC Q9H229: 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE C-type lectin DB27 short form.
GN DB27.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RP Richard M., Beaulieu A.D.:
RT "A short ORF for the C-type lectin DB27."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF200736; AAG35593.1; -
DR InterPro: IPR002353; Antifreeze1.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C.1.
DR PRINTS: PR000356; ANTI-FREEZE1.
DR SMART: SM00034; CLECT.1.
DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
SQ SEQUENCE 204 AA; 23550 MW; 4DFPC27549CEBA5 CRC64;

Query Match 84.3%; Score 1079.5; DB 4; Length 204;
Best Local Similarity 85.7%; Pred. No. 2.5e-97;
Matches 203; Conservative 1; Mismatches 0; Indels 33; Gaps 1;

QY 1 MTSETTVAEVRPKNEFKSSGINTASSAKERTAPLKNTPGPKLLCASILTFLLAIS 60
DB 1 MTSETTVAEVRPKNEFKSSGINTASSAKERTAPLKNTPGPKLLCASILTFLLAIS 60
QY 61 FFIAFVIFFOKYSQLEKRTTKELVHTTLECYKKNMPYETAMSCCPKNNKSFSSNCYFI 120
DB 61 FFIAFVIFFOKYSQLEKRTTKELVHTTLECYKKNMPYETAMSCCPKNNKSFSSNCYFI 120
QY 121 STESASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORHOMWD 180
DB 121 STESASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORHOMWD 180
QY 88 STESASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORHOMWD 147
DB 88 STESASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORHOMWD 147
QY 181 QTPYNESSTFWHPRPSDPNERCVLNFRRKSPKRGWMDVNCIGPORSVCEMMKTHL 237
DB 181 QTPYNESSTFWHPRPSDPNERCVLNFRRKSPKRGWMDVNCIGPORSVCEMMKTHL 237

RESULT 6

Q9Q215 PRELIMINARY: PRT: 238 AA.
AC Q9Q215: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Dendritic cell immunoreceptor (C-type).
GN CLEC5F OR DCIR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Lymph node.
RX MEDLINE-99370001; PubMed-10436934;
RA Bates E.E., Fournier N., Garcia E., Valladeau J., Durand I., Pan J.J.,
RA Zurawski S.M., Patel S., Abrams J.S., Lebecque S., Garrone P.,
RA Saeland S.;
RT "Apc8 express DCIR, a novel C-type lectin surface receptor containing
an immunoreceptor tyrosine-based inhibitory motif."
RL J. Immunol. 163:1973-1983(1999).
[2]

RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c;
RX MEDLINE-21830942; PubMed-11841542;
RA Kanazawa N., Okazaki T., Nishimura H., Tashiro K., Inaba K.,
RA Miyachi Y.;
RT "DCIR acts as an inhibitory receptor depending on its immunoreceptor
tyrosine-based inhibitory motif."
RL J. Invest. Dermatol. 118:261-266(2002).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-Cerebellum;
RX MEDLINE-22354683; PubMed-12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:565-573(2002).
DR EMBL: AJ133533; CAB57870.1; -
DR EMBL: AF387099; AAM22402.1; -
DR EMBL: AK049002; BAC33509.1; -
DR HSSP: P05140; ZAFP.
DR MGI: 1349412; Clec5f6.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C.1.
DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 238 AA; 27323 MW; 2DB8AE0E11B18A56 CRC64;

Query Match 52.5%; Score 672.5; DB 11; Length 238;
Best Local Similarity 53.3%; Pred. No. 1.5e-57;
Matches 129; Conservative 37; Mismatches 67; Indels 9; Gaps 6;

QY 1 MTSETTVAEVRPKNEFKSSGINTASSAKERTAPLKS--NTGPKLLCASILTFLLAIS 58
DB 1 MTSETTVAEVRPKNE--SNSLHTYESPAAPREKPIRDLRRKGPSLLTSLMLLLILA 58
QY 59 ISFFIAFVIFFOKYSQLEKRTTKELVHTTLECYKKNMPYETAMSCCPKNNKSFSSNC 117
DB 59 ITFLVAFVIFFOKYSQLEKRTTKELVHTTLECYKKNMPYETAMSCCPKNNKSFSSNC 117
QY 118 YFIST--ESASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORH 175
DB 118 YFIST--ESASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORH 175
QY 119 YLVTYSSASWKNKSEKNSRGMALHYIQSQEDDITGLIDTAHAFFIGLMD-TGHRQ 177
DB 119 YLVTYSSASWKNKSEKNSRGMALHYIQSQEDDITGLIDTAHAFFIGLMD-TGHRQ 177
QY 176 WQWVDQTPYNESSTFWHPRPSDPNERCVLNFRRKSPKRGWMDVNCIGPORSVCEMMKTI 235
DB 176 WQWVDQTPYNESSTFWHPRPSDPNERCVLNFRRKSPKRGWMDVNCIGPORSVCEMMKTI 235
QY 236 HL 237
DB 236 HL 237

QY 237 NL 238
DB 237 NL 238

RESULT 7

Q923C7 PRELIMINARY: PRT: 262 AA.
AC Q923C7: 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Similar to C-type (calcium dependent, carbohydrate recognition domain)

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DE lectin, superfamily member 6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10950;
RN (1)
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC006623; AA06623.1; -.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 262 AA; 29822 MW; 413DAD69511071B8 CRC64;

Query Match 50.8%; Score 650.5; DB 11; Length 262;
St Local Similarity 48.5%; Pred. No. 2,3e-55;
tches 129; Conservative 37; Mismatches 67; Indels 33; Gaps 7;

QY 1 MTSIITYAEVREKFKSSGINTASSASKERTAPLKS--NTGPKILCASLLIFELLAA 58
DB 1 MASEIYAEVKEKNE--SNSLHTSSESPAPREKPIRLDRKPSPLSLTSLMLLLLLA 58
QY 59 ISEFIAPVIFPKYSOLL-EKTTKELVHTTECVKKNMPV----- 98
DB 59 IIFLVAFIIFYFKYSOLLLEKKAKNIMHNLCTKSVPMEAPPIGORALTLESIEIDL 118
QY 99 -----ETAMSCCPKMKKSFSSNCYFISF--ESASQDESKDCARMEAHLLVINTOEOD 151
DB 119 GILAPDKVWSCCPKRLFGSHCYLVPYSSASNNKSEENCSRMGAHLVYQSODED 178
QY 152 FIFONLQESSAFVGLSDPEGQRHMQVDPYNESTFWHPREPSDNERCVLNFERS 211
DB 179 FITGILDTHAAYTIGLMD-TGHRQWQVQOTPEESITTHNHPSPSSGNKCAITTYRK 237
QY 212 PKRMGNVNCUGAPQPSVCEMKIHL 237
DB 238 -TGMGNWDISCSLKQSVCKMKIHL 262

RESULT 8
Q8WTT0 PRELIMINARY; PRT; 213 AA.
Q8WTT0; 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Dendritic lectin (Blood dendritic cell antigen 2 protein).
GN CLECSF11 OR BDCA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE-21426806; PubMed-11536172;
RA Arce I., Roda-Navarro P., Montoya M.C., Hernanz-Falcon P.,
RA Pulg-Krieger A., Fernandez-Rulz E.;
RT "Molecular and genomic characterization of human DLEC, a novel member
RT of the C-type lectin receptor gene family preferentially expressed on
RT monocyte-derived dendritic cells.";
RT Eur. J. Immunol. 31:2733-2740(2001).
RN (2)
RP SEQUENCE FROM N.A.
RA Schme Y., Johnston I., Dzionek A., Nagasaka T., Nagafune J., Okada T.,
RA Hirano T., Schmitz J., Yamaguchi Y.;
RT "Cloning and characterization of blood dendritic cell antigen 2 (BDCA-
RT 2), a C-type lectin expressed on plasmacytoid dendritic cells.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF325459; AAL37358.1; -.
DR EMBL: AF293615; AAL37036.1; -.

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DR Genew; HGNC:14557; CLECSF11.
DR InterPro: IPR002353; AntifreezeZell.
DR InterPro: IPR003854; GASA.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF02704; GASA; 1.
DR Pfam: PF00059; Lectin_C; 1.
DR PRINTS: PR00356; ANTIFREEZEII.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
KM lectin.
SQ SEQUENCE 213 AA; 25037 MW; 5DC82C95BE2378C1 CRC64;

Query Match 43.1%; Score 551.5; DB 4; Length 213;
Best Local Similarity 50.8%; Pred. No. 8.4e-46;
Matches 97; Conservative 38; Mismatches 49; Indels 7; Gaps 3;

QY 51 LIFELLALISFIAFYI----FFQKISQLLEKTTKELVHTTECVKKNMPVETAMSCC 106
DB 26 VVSILLVCFTVSVVPHNFMYSKTRLSKIREYQYQYHPSLTQVMEKDIED--WSCC 83
QY 107 PKMKKSFSSNCYFISTESASQDESKDCARMEAHLLVINTOEODPIFONLQESSAFVG 166
DB 84 PTPWTFQSSCFITSTGMSQSWTSQKNCVGMADLVVINTREODPIONLKNSSYFLG 143
QY 167 LSDPEGQRHMQVDPYNESTFWHPREPSDNERCVLNFERSPKRMGNVNCUGPO 226
DB 144 LSDPGRHRHMQVDPYNESTFWHSGBPNNIDERCALINFRSS-EEWGMNDIHCHVPO 202
QY 227 RSYCEMKIHL 237
DB 203 KSIQKMKKIYI 213

RESULT 9
Q8WXX8 PRELIMINARY; PRT; 182 AA.
Q8WXX8; 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Dendritic lectin b isoform.
GN CLECSF11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE-21426806; PubMed-11536172;
RA Arce I., Roda-Navarro P., Montoya M.C., Hernanz-Falcon P.,
RA Pulg-Krieger A., Fernandez-Rulz E.;
RT "Molecular and genomic characterization of human DLEC, a novel member
RT of the C-type lectin receptor gene family preferentially expressed on
RT monocyte-derived dendritic cells.";
RT Eur. J. Immunol. 31:2733-2740(2001).
RL EMBL: AF325460; AAL37359.1; -.
DR InterPro: IPR002353; AntifreezeZell.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C; 1.
DR PRINTS: PR00356; ANTIFREEZEII.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
KM lectin.
SQ SEQUENCE 182 AA; 21498 MW; 78BE4EAE0109FAE7 CRC64;

Query Match 41.7%; Score 533.5; DB 4; Length 182;
Best Local Similarity 54.4%; Pred. No. 4e-44;
Matches 92; Conservative 31; Mismatches 43; Indels 3; Gaps 2;

QY 69 FQKISQLLEKTTKELVHTTECVKKNMPVETAMSCCCKKMKKSFSSNCYFISTESASQ 128

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[illegible]

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AC      08J2X6; 22, Last sequence update)
DT      01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT      01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      RIKEN CDNA 3110037K17 gene.
GN      3110037K17Rik.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Mammary gland;
RA      Strauberg R.;
RL      Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC034893; AAH34893.1; -
DR      MGD; MGI:1920399; 3110037K17Rik.
DR      InterPro; IPR002353; Antifreezeell.
DR      InterPro; IPR001969; Aspartatease-site.
DR      InterPro; IPR001304; Lectin_C.
DR      Pfam; PF00059; lectin_c_1.
DR      PRINTS; PRO0356; ANTIFREEZEELI.
DR      SMART; SMO0034; CLECT_1.
DR      PROSITE; PS00141; ASP_PROTEASE_1.
DR      PROSITE; PS00615; C-TYPE_LECTIN_1.
DR      PROSITE; PS50041; C-TYPE_LECTIN_2_1.
SQ      SEQUENCE 158 AA; 18325 MW; B34D8A4FEDA4F76B CRC64;

Query Match          37.2%; Score 476.5; DB 11; Length 158;
Best Local Similarity 53.5%; Pred. No. 1.2e-38;
Matches 84; Conservative 30; Mismatches 40; Indels 3; Gaps 3

QY      VYVHTLECYCKKKMPVEETAMSCCPKKMKSFSSNCRISTE-SASMODEKDCARMEAH 140
Db      4 KELYATTELCRKMAISLEDKWKMSCPKMKRFSGCYTSTSDIVASNMESKNCCHMGH 63
QY      141 LVLINTOEEDDFIFONTQEESAYTVGLSDPEGQRHWQWVDOTPVNESSTFWHPRESPDN 200
Db      64 LVVHSOEOEPFIGILDTGTAFYFLGSLNP-GDOOWMWDITPPYDNTTFWHKGEPSSDN 122
QY      201 ERCVYLNFRRKSPKRGMWDNVCLGPQRSVCSEMRKTHL 237
Db      123 EQCVLIINHROS-TGWMGMSDIPCSDKONSICHHKIYL 158

RESULT 12
O9JKF3 PRELIMINARY; PRT; 175 AA.
AC      O9JKF3;
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Dectln-2 beta isoform.
DE      Dectln-2 beta isoform.
CN      CLEC3F10.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c;
RA      Arizumi K., Shen G., Shikano S., Rlter R. II, Zukas P.,
RA      Edellaum D., Morita A., Takashima A.;
RT      "Cloning of a second dendritic cell-associated C-type lectin (dectln-
RT      2) and its alternatively spliced isoforms."
RL      J. Biol. Chem. 0:0-0(2000);
DR      EMBL; AF240358; AAF67178.1; -
DR      HSSP; P22897; LEGG.
DR      MGD; MGI:1861231; Clec3f10.
DR      InterPro; IPR001304; Lectin_C.
DR      Pfam; PF00059; lectin_c_1.
DR      SMART; SMO0034; CLECT_1.
DR      PROSITE; PS00615; C-TYPE_LECTIN_1_1.
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Query Match	35.4%	Score 452.5	DB 11	Length 175
Best Local Similarity	43.4%	Pred. No. 3,1e-36		
Matches	82	Conservative	28	Mismatches 46; Indels 33; Gaps 3
Qy	49	SLIIFELLATSPFAVIFPFQKYSQLEKKTTRKELVHTLTLCVKKNNPVEETAMSCCPK	108	
Db	20	SAAVISMLLSCTFLA-----SCVKK-----MGCCPN	47	
Qy	109	NKSFSSNCYFIESTESAMODESKCAMEAHLVINTQEDDFIFQNLQESAFYGLS	168	
Db	48	HMSGSGSCCISTSTENFWSTSEQCYMGALHVIINTEAGDNFTLQNLBSLSTFLGLS	107	
Qy	169	DPEGGRKQWVDQPPYNESSSTFWHREPSDPNERCVINLFRKSPKRGWMDVNCIGPORS	228	
Db	108	DPOGNGKQWQIDDPFESQVRFWRHPEHNPDLPEERCVSIVY-WNPSKGMGMDVFCDSKHS	166	
Dd	229	VCEMKKIKL	237	
	167	ICEMKKIYL	175	
RESULT 13				
Q9DB07				
ID	Q9DB07	PRELIMINARY:	PRT:	176 AA.
AC	Q9DB07			
DT	01-JUN-2001	(TREMBLrel. 17, Created)		
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)		
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)		
DE	1810046124Rik	protein.		
GN	1810046124Rik.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NC	NCBI_Taxid=10090;			
TX	[1]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=C57BL/6J; TISSUE=Pancreas;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shingawa A.A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,			
RA	Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Futuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoendach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,			
RA	Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,			
RA	Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection."			
RL	Nature 409:665-690(2001).			
DR	EMBL; AK007794; BABS260.1; -			
DR	HSSP; P05140; 2AEP.			
DR	MCD; MGI:1917060; 1810046124Rik.			
DR	InterPro: IPR001304; Lectin_C.			
DR	Pfam: PF00059; Lectin_C.1.			
DR	SMART; SM00034; CLECT; 1.			
DR	PROSITE; PS00615; C-type_LECTIN_1; 1.			
DR	PROSITE; PS0041; C-type_LECTIN_2; 1.			
SO	SEQUENCE 176 AA; 20342 MW; C020F49633D27BA CRC64;			
Query Match	34.9%	Score 447	DB 11	Length 176
Best Local Similarity	46.6%	Pred. No. 1,1e-35		

Matches	89: Conservative	24: Mismatches	42: Indels	36: Gaps	5
OY	49 SLIFPELLAISFPAFYIFFOKYSQLLLEKTKTKELVHTTELCYKKNPVEETANSCCK	108			
Db	20 SAAVYISILLSTCFIA-----SCVDR-----VWSCCK	47			
OY	109 NAKSPSSNCYFIST--ESASMODESKDCARMEAHLLVINTOEOPFIFONLOEESAYFVG	166			
Db	48 DMKLEFGSICLYLPVYFSSASNNKSENCRMAHLYVHSODEOPFITGILDTHAAYFIG	107			
OY	167 LSDEGQRHOMQVDDTPYNESSTFWHPREPSDPNRCVYLNFRKSPKRGWMDVNCLO	226			
Db	108 LMD-TGHRQWQVDDTPYEEASTVFPHNEBPSSDNEKCYTVYRRN-IGWMDISCNLKQ	165			
OY	227 KSVCEMAKITHL 237				
Db	166 KSVCKMKKINL 176				
RESULT 14					
O8CIG3	PRELIMINARY;	PRT;	152 AA.		
ID	O8CIG3				
AC	O8CIG3;				
DT	01-MAR-2003 (TREMBLrel. 23, Created)				
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE	C-type (Fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID	10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Epididymis;				
RX	MEDLINE=22354683; PubMed=12466851;				
RA	The FANTOM Consortium,				
RA	The RIKEN Genome Exploration Research Group Phase I & II Team;				
RT	"Analysis of the mouse transcriptome based on functional annotation of				
RL	60,770 full-length cDNAs."				
DR	Nature 420:563-573(2002).				
FT	EMBL; AK020363; BAC25626.1; -				
NON_TER	1				
SO	SEQUENCE 152 AA; 17489 MW; 5A9646BC29FD834B CRC64;				
Query Match					
	34.4%; Score 440.5; DB 11; Length 152;				
	Best Local Similarity 52.6%; Pred. No. 3.9e-35;				
Matches	81; Conservative 25; Mismatches 41; Indels 7; Gaps 4				
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Db	1 LESIEIIDGILAPBEKRVKSCCPDMKRLFGSHCYLPVYSSSASNNKSENCRMAHLLV	60			
OY	144 INFOEOPFIFONLOEESAYFVGSLDPEGRHOMQVDDTPYNESSTFWHPREPSDPNRC	203			
Db	61 IQSODEOPFITGILDTHAAYFIGLMD-TGHRQWQVDDTPYEEASTVFPHNEBPSGNGENC	119			
OY	204 VLVNFRKSPKRGWMDVNCLOPORSVCMAKITHL 237				
Db	120 ATIIYRWK-TGWMGDNDISCSLKQSKVCQMKKINL 152				
RESULT 15					
O8NSJ5	PRELIMINARY;	PRT;	215 AA.		
ID	O8NSJ5				
AC	O8NSJ5;				
DT	01-OCT-2002 (TREMBLrel. 22, Created)				
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE	C-type lectin-like receptor.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
NCBI_TaxID	9606;				

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 12:55:42 ; Search time 85 Seconds

(without alignments)
442.567 Million cell updates/sec

Title: US-09-862-802-2

Perfect score: 1280

Sequence: 1 MTSEITYAEVFRKNEFKSSG.....NDVNCIGPQRSCVCEMMKTHL 237

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1280	100.0	237	20	AAW88124
2	1275	99.6	237	23	ABB90277
3	1273	99.5	237	22	AAU98014
4	1267	99.0	243	22	AAU98014
5	1267	99.0	243	23	ABP48034
6	1267	99.0	246	22	AAU19653
7	1267	99.0	246	23	ABP4/873
8	1059.5	82.8	198	23	ABP63043
9	672.5	52.5	238	20	AAW88128

10	552	43.1	211	22	AAE12080
11	551.5	43.1	213	23	AAE84215
12	551.5	43.1	213	22	AAE27987
13	551.5	43.1	218	22	AAE12079
14	534.5	41.8	182	23	AAE27988
15	507.5	39.6	134	23	AAU98013
16	507.5	39.6	148	23	AAU98015
17	489	38.2	209	19	AAW63010
18	489	38.2	209	19	AAU27447
19	489	38.2	209	22	AAU00482
20	473.5	37.0	167	19	AAW63022
21	458	35.8	209	22	AAU00479
22	452.5	35.4	145	19	AAW63017
23	452.5	35.4	175	19	AAW63018
24	356	27.8	59	23	ABG80759
25	335.5	26.2	162	20	AAU27446
26	330.5	25.8	168	19	AAW63020
27	330	25.8	219	20	AAU13403
28	330	25.8	219	22	AAU29035
29	330	25.8	219	22	AAU29035
30	330	25.8	219	22	AAU29035
31	330	25.8	219	22	AAU29035
32	330	25.8	219	24	ABU69681
33	330	25.8	219	24	ABU71123
34	330	25.8	219	24	ABU71504
35	330	25.8	219	24	ABU71950
36	330	25.8	219	24	ABU65580
37	330	25.8	219	24	ABU65913
38	330	25.8	219	24	ABU67404
39	330	25.8	219	24	ABU67417
40	330	25.8	219	24	ABU64558
41	330	25.8	219	24	ABU65275
42	330	25.8	219	24	ABU58411
43	330	25.8	219	24	ABU55947
44	330	25.8	219	24	ABU56942
45	330	25.8	219	24	ABU34406
					ABU10521

ALIGNMENTS

RESULT 1	
AAW88124	AAW88124 standard; Protein; 237 AA.
XX	XX
AC	AAW88124;
XX	XX
DT	11-MAY-1999 (first entry)
XX	XX
DE	Primate DCMPI C-lectin family gene protein sequence.
XX	XX
KW	Primate: dendritic cell membrane protein; DCMPI; DCMPI;
KW	Chromosomal abnormality; expression misregulation;
KW	abnormal proliferation; regeneration; degeneration; haematopoietic cell.
OS	Mammalia.
XX	XX
PN	WO9902562-A1.
XX	XX
PD	21-JAN-1999.
XX	XX
PF	08-JUL-1998; 98MO-US1436.
XX	XX
PR	09-JUL-1997; 97US-0053080.
XX	XX
PA	(SCHE) SCHERING CORP.
XX	XX
PI	Bates EM, Ford J, Lebeque SE, Ravel O, Saeland S;
PI	Valladeau J;
XX	XX
DR	WPI: 1999-120786/10.
DR	N-PSDB: AAX04865.
XX	XX

PT Dendritic cell membrane proteins - used to treat conditions
PT associated with abnormal physiology or development
XX
PS Claim 1; Page 65-66; 82pp; English.
XX
CC Dendritic cell membrane protein 1 (DCMP1) and DCMP2 nucleic acids can be
CC used as markers for distinguishing cell types, including genomic aspects
CC of cells, as well as mRNA and protein expression patterns. They can also
CC be used to detect chromosomal abnormalities. The proteins can be used to
CC diagnose disorders associated with expression misregulation. They can
CC also be used to treat conditions associated with abnormal physiology or
CC development, including abnormal proliferation, e.g. cancerous conditions
CC or degenerative conditions. Abnormal proliferation, regeneration,
CC degeneration and atrophy may be modulated using the proteins. The
CC proteins may also play a role in regulation or development of
CC hematopoietic cells.
XX
SQ Sequence 237 AA;
XX
Query Match 100.0%; Score 1280; DB 20; Length 237;
Best Local Similarity 100.0%; Pred. No. 6.7e-127;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MTSKITAEVFRNFKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFPELLAIS 60
Db 1 MTSKITAEVFRNFKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFPELLAIS 60
QY 61 FFLAFVFFQKYSQLEKTKTKELVHTTECVKKNMPEETANSCCPKNNKSSSNCYFI 120
Db 61 FFLAFVFFQKYSQLEKTKTKELVHTTECVKKNMPEETANSCCPKNNKSSSNCYFI 120
QY 121 STESASWQDEKDCARMEHLVINTQEBODFTFQNIQESAFVGLSDPEGORHQMWD 180
Db 121 STESASWQDEKDCARMEHLVINTQEBODFTFQNIQESAFVGLSDPEGORHQMWD 180
QY 181 QTPYNESSTFWHPRESDPNERCYVILNFRKSPKRWGNDVNCIGPORSVCENMKIHL 237
Db 181 QTPYNESSTFWHPRESDPNERCYVILNFRKSPKRWGNDVNCIGPORSVCENMKIHL 237
XX
RESULT 2
AB90277
ID ABB90277 standard; Protein: 237 AA.
XX
AC ABB90277;
XX
24-MAY-2002 (first entry)
XX
Human polypeptide SEQ ID NO 2653.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US16450.
XX
PR 19-MAY-2000; 2000US-205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-122018/16.
XX
N-PDB; ABL90686.
XX

PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders -
XX
PS Claim 11; SEQ ID NO 2653; 2081pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABL989449-ABL90853) and proteins
CC (AB989040-AB990444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at http://wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 237 AA;
XX
Query Match 99.6%; Score 1275; DB 23; Length 237;
Best Local Similarity 99.6%; Pred. No. 2.3e-126;
Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 MTSKITAEVFRNFKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFPELLAIS 60
Db 1 MTSKITAEVFRNFKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFPELLAIS 60
QY 61 FFLAFVFFQKYSQLEKTKTKELVHTTECVKKNMPEETANSCCPKNNKSSSNCYFI 120
Db 61 FFLAFVFFQKYSQLEKTKTKELVHTTECVKKNMPEETANSCCPKNNKSSSNCYFI 120
QY 121 STESASWQDEKDCARMEHLVINTQEBODFTFQNIQESAFVGLSDPEGORHQMWD 180
Db 121 STESASWQDEKDCARMEHLVINTQEBODFTFQNIQESAFVGLSDPEGORHQMWD 180
QY 181 QTPYNESSTFWHPRESDPNERCYVILNFRKSPKRWGNDVNCIGPORSVCENMKIHL 237
Db 181 QTPYNESSTFWHPRESDPNERCYVILNFRKSPKRWGNDVNCIGPORSVCENMKIHL 237
XX
RESULT 3
AAU98014
ID AAU98014 standard; Protein: 237 AA.
XX
AC AAU98014;
XX
27-AUG-2002 (first entry)
XX
Human dendritic cell immunoreceptor AU133532.
XX
XX Human: dendritic cell immunoreceptor; cytostatic;
KW antiasthmatic; anorectic; antidiabetic; cancer; allergy; anaphylaxis;
KW asthma; inflammation; obesity; diabetes; central nervous system disorder;
KW Alzheimer's disease; Parkinson's disease; dementia; osteoarthritis;
KW cardiovascular disorder; myocardial infarction; ischemic heart disease;
KW congestive heart failure; chronic obstructive pulmonary disease; COPD.
XX
OS Homo sapiens.
XX
PN WO200232958-A2.
XX
PD 25-APR-2002.
XX
PF 12-OCT-2001; 2001WO-EP11812.
XX

XX 16-OCT-2000; 2000US-240096P.
PR 27-AUG-2001; 2001US-314651P.
XX (FARB) BAYER AG.
PA Smolyar A;
XX WPI; 2002-463308/49.
XX Novel human dendritic cell immunoreceptor polypeptide, useful for
PT treating cancer, asthma, obesity, diabetes, central nervous system
PT disorder or cardiovascular disorder
XX
XX Disclosure; Fig 3; 11app; English.
XX The invention relates to a purified human dendritic cell immunoreceptor
CC polypeptide and its encoding nucleic acid. Also included are an
CC expression vector comprising the nucleic acid, a host cell containing
CC the vector, reducing the activity of human dendritic cell immunoreceptor
CC involves contacting a cell with a reagent which specifically binds to
the polypeptide or nucleic acid and a reagent that modulates the activity
of the polypeptide or nucleic acid. The reagent is useful for the
preparation of a medicament for modulating the activity of human
dendritic cell immunoreceptor in a disease such as cancer, allergy,
CC anaphylaxis, asthma, inflammation, obesity, diabetes, a central nervous
CC system (CNS) disorder (e.g. Alzheimer's disease, Parkinson's disease or
dementia), or a cardiovascular disorder (e.g. myocardial infarction,
CC ischemic heart disease, congestive heart failure), chronic obstructive
CC pulmonary disease (COPD) and osteoarthritis (many other diseases and
CC disorders are listed in the specification). The polypeptide and nucleic
CC acid are useful for identifying test compounds which act as agonists or
CC antagonists, for raising specific antibodies, and as a bait protein in a
CC two-hybrid or three-hybrid assay. The nucleic acid is useful in
CC diagnostic assays for detecting diseases and abnormalities or
CC susceptibility to disease and abnormalities related to the presence of
CC mutations. The present sequence represents a dendritic cell
CC immunoreceptor from Genbank accession number AJ133532.
XX
XX Sequence 237 AA;
SQ
Query Match 99.5%; Score 1273; DB 23; Length 237;
Best Local Similarity 99.6%; Pred. No. 3,7e-126;
Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTSITTAEVFRKNEFKSSGINTASSAASKERTAPLKSNTGFPPLDASLIIFLLAIS 60
Dh 1 MTSITTAEVFRKNEFKSSGINTASSAASKERTAPLKSNTGFPPLDASLIIFLLAIS 60
61 FFIAFVIFPQKYSQLEKTKTKELVHTTLECVKKNMVEEFTAMSCCPKNNKSPSSNCYFT 120
Dh 61 FFIAFVIFPQKYSQLEKTKTKELVHTTLECVKKNMVEEFTAMSCCPKNNKSPSSNCYFT 120
QY 121 STESASWQDSEKDCARMEAHLLVINTQEDDFIPONLOESAVYFVGSDEGQRHMQWD 180
Dh 121 STESASWQDSEKDCARMEAHLLVINTQEDDFIPONLOESAVYFVGSDEGQRHMQWD 180
QY 121 STESASWQDSEKDCARMEAHLLVINTQEDDFIPONLOESAVYFVGSDEGQRHMQWD 180
QY 181 QTPVNESSTFMHREPDPNERCVLNFKRSFKRWGNNDVNCGLGPOSSVCEMAKITHL 237
Dh 181 QTPVNESSTFMHREPDPNERCVLNFKRSFKRWGNNDVNCGLGPOSSVCEMAKITHL 237
181 QTPVNESSTFMHREPDPNERCVLNFKRSFKRWGNNDVNCGLGPOSSVCEMAKITHL 237
RESULT 4
AAU19814
ID AAU19814 standard; Protein: 243 AA.
XX AAU19814;
AC
XX
DT 04-DEC-2001 (first entry)
XX
DE Human novel extracellular matrix protein, Seq ID No 464.
XX
KW Human; secreted extracellular matrix protein; immunomodulatory;

KW Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; vascular;
KW cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cyostatic;
KW antialzheimers; immune/autoimmune disease; HIV infection; anaemia;
KW human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;
KW cancers; hyperproliferative disorder; breast neoplasm; melanoma;
KW Sezary syndrome; Gaucher's disease; neurological diseases;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
KW cardiac arrest; tachycardia; angina; infection; corneal infections;
KW wound healing; immunogen; gene therapy; antisense; food additive.
OS Homo sapiens.
XX W020015368-A1.
XX
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WC-US01348.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 06-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.

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PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
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PR 26-SEP-2000; 2000US-0235484.
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PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 02-OCT-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0238937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
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PR 08-NOV-2000; 2000US-0246610.
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PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.

PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI: 2001-465572/50.
DR N-PSDB; AAS31385.
XX
PT Nucleic acid molecules encoding human secreted extracellular matrix
PS proteins, used in preventing, treating or ameliorating a disorder, e.g.
XX Alzheimer's and Parkinson's diseases and cancers -
PS
XX Claim 11; SEQ ID No 464; 577pp; English.
CC The invention relates to isolated nucleic acid molecules encoding
CC novel human secreted extracellular matrix proteins (SPs). The
CC polynucleotides and proteins are used to prevent, treat a medical
CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
CC chickens or sheep. For example, disorders associated with decreased
CC expression of SPs. The SP polynucleotide or a vector expressing them may
CC be administered to treat diseases by gene therapy. Antisense molecules
CC may be administered to down regulate expression of SPs by binding with
CC the cells own genes and preventing their expression. The polynucleotides
CC may also be used as DNA probes in diagnostic assays. The SPs may also be
CC used as antigens to produce antibodies and to identify modulators
CC (agonists and antagonists) of the SPs. The anti-(SP) antibodies and
CC antigens may also be used to down regulate expression and activity of
CC SP and as diagnostic agents for detecting the presence of SPs in samples.
CC The disorders include for example: immune/autoimmune diseases (e.g. HIV
CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
CC and multiple sclerosis), cancers and hyperproliferative disorders (e.g.
CC melanomas, neoplasms of the breast or liver, Sezary syndrome and
CC Gaucher's disease), neurological diseases (e.g. Alzheimer's disease,
CC Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac
CC arrest, tachycardia and angina), infections caused by bacteria, viruses
CC and fungi and ocular disorders (e.g. corneal infections). Other uses
CC include wound healing, maintenance of organs before transplantation,
Query Match 99.0%; Score 1267; DB 22; Length 243;
Best Local Similarity 99.6%; Pred No. 1.6e-125;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 3 SEITAEVFRKNEFKSSGINTASSAASKERTAPLKSNTGFPRLCALSILIFLLAISFF 62
DB 9 AEITAEVFRKNEFKSSGINTASSAASKERTAPLKSNTGFPRLCALSILIFLLAISFF 68
OY 63 IAFVIFPQKYSOLEKTKTKELVHTTLEEVKKNMVEEERAWSCCPKNNKSFSSNXYFIST 122
DB 69 IAFVIFPQKYSOLEKTKTKELVHTTLEEVKKNMVEEERAWSCCPKNNKSFSSNXYFIST 128
OY 123 ESASWDSKDCARMEAHLLVINTOEEDOFIIONIOESASVYVGSDESGRHHMOWVOT 182
DB 129 ESASWDSKDCARMEAHLLVINTOEEDOFIIONIOESASVYVGSDESGRHHMOWVOT 188
OY 183 PYNESSTFWHPREPSDPNERCVLVNFRKSPKMGNDVNCJLGPORSVCEMMKIH 237
DB 189 PYNESSTFWHPREPSDPNERCVLVNFRKSPKMGNDVNCJLGPORSVCEMMKIH 243
RESULT 5
ABP48034 ID ABP48034 standard; Protein; 243 AA.
XX AC ABP48034;
XX

DT 23-AUG-2002 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 464.
 XX
 KW Human; nootropic; neuroprotective; cytoskeletal; dermatological; virucide;
 KW immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnery;
 KW antiparkinsonian; antischizoid; antianemic; antithrombotic; cancer;
 KW antirheumatic; hepatoprotective; cerebroprotective; anti-inflammatory;
 KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
 KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2002042386-A1.
 XX
 PD 11-APR-2002.
 XX
 PF 17-JAN-2001; 2001US-0764870.
 XX
 PR 31-JAN-2000; 2000US-179065P.
 PR 04-FEB-2000; 2000US-180628P.
 PR 28-JUN-2000; 2000US-214886P.
 PR 07-JUL-2000; 2000US-216647P.
 PR 07-JUL-2000; 2000US-216880P.
 PR 11-JUL-2000; 2000US-217487P.
 PR 11-JUL-2000; 2000US-217496P.
 PR 14-JUL-2000; 2000US-218290P.
 PR 26-JUL-2000; 2000US-220963P.
 PR 26-JUL-2000; 2000US-220964P.
 PR 14-AUG-2000; 2000US-224518P.
 PR 14-AUG-2000; 2000US-224519P.
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 PR 14-AUG-2000; 2000US-225477P.
 PR 14-AUG-2000; 2000US-225757P.
 PR 14-AUG-2000; 2000US-225758P.
 PR 22-AUG-2000; 2000US-226688P.
 PR 30-AUG-2000; 2000US-228924P.
 PR 01-SEP-2000; 2000US-229287P.
 PR 01-SEP-2000; 2000US-229343P.
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 PR 05-SEP-2000; 2000US-229509P.
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 PR 08-SEP-2000; 2000US-231413P.
 PR 21-SEP-2000; 2000US-234223P.
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 PR 25-SEP-2000; 2000US-234997P.
 PR 27-SEP-2000; 2000US-235834P.
 PR 29-SEP-2000; 2000US-236327P.
 PR 29-SEP-2000; 2000US-236367P.
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 PR 02-OCT-2000; 2000US-236802P.
 PR 02-OCT-2000; 2000US-237037P.
 PR 02-OCT-2000; 2000US-237038P.
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 PR 20-OCT-2000; 2000US-241785P.
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 PR 01-NOV-2000; 2000US-244617P.
 PR 17-NOV-2000; 2000US-249299P.
 PR 08-DEC-2000; 2000US-251856P.
 PR 08-DEC-2000; 2000US-251868P.
 PR 08-DEC-2000; 2000US-251869P.
 XX
 XX
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC.
 XX
 DR WPI: 2002-470713/50.
 DR N-PSDB; AB066709.
 XX
 PT New nucleic acid encoding human proteins, useful for diagnosis,
 PT treatment and prevention of e.g. osteoporosis, also related
 XX polypeptides and antibodies
 PS
 PS Claim 11; SEQ ID NO 464; 235pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (AB066521-AB066785) and proteins
 CC (ABP47846-ABP48110) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html?docID=999909764870.
 XX
 SQ Sequence 243 AA:
 XX
 Query Match 99.0%; Score 1267; DB 23; Length 243;
 Best Local Similarity 99.6%; Pred. No. 1.6e-125;
 Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 3 SEITTAEVKFKNEFSSGINTASSAASKRTAPLKSNTGPKLLCASLIFLLAISFF 62
 DB :|||||
 DB 9 AEITTAEVKFKNEFSSGINTASSAASKRTAPLKSNTGPKLLCASLIFLLAISFF 68
 QY 63 IAFVIFFOKYSOLLEKTKKELVHTLLECVKNNMPEETAWSCCPKNNKSFSSNCYFIST 122
 DB :|||||
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 DB :|||||
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 DB :|||||
 DB 189 PYNESSTFWHPREPSDPNERCVVNLNFKSPKRWGNDVNCGLPQNSVCEMKIHL 243
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 RESULT 6
 ID AAU19653
 ID AAU19653 standard; Protein: 246 AA.
 XX
 AC AAU19653;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE Human novel extracellular matrix protein, Seq ID No 303.
 XX
 DE Human; secreted extracellular matrix protein; immunomodulatory;
 KW Anti-HIV; antianemic; antirheumatic; antischlerotic; cardiac; vascular;
 KW cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytoskeletal;
 KW antiallergic; immune/autoimmune disease; HIV infection; anaemia;
 KW human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;
 KW cancers; hyperproliferative disorder; breast neoplasm; melanoma;
 KW Searzy syndrome; Gaucher's disease; neurological diseases;
 KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;

KM cardiac arrest; tachycardia; angina; infection; corneal infections;
wound healing; immunogen; gene therapy; antisense; food additive.
XX Homo sapiens.
XX WO200155368-A1.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01348.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
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PR 19-MAY-2000; 2000US-0205515.
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PR 17-NOV-2000; 2000US-0249217.
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PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.

PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465572/50.
DR N-PSDB; AAS31224.
XX
XX Nucleic acid molecules encoding human secreted extracellular matrix
PR proteins, used in preventing, treating or ameliorating a disorder, e.g.
PT Alzheimer's and Parkinson's diseases and cancers.
XX
XX
XX Claim 11; SEQ ID No 303; 577pp; English.
XX
XX The invention relates to isolated nucleic acid molecules encoding
CC novel human secreted extracellular matrix proteins (SPs). The
CC polynucleotides and proteins are used to prevent, treat a medical
CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
CC chickens or sheep. For example, disorders associated with decreased
CC expression of SPs. The SP polynucleotide or a vector expressing them may
CC be administered to treat diseases by gene therapy. Antisense molecules
CC may be administered to down regulate expression of SPs by binding with
CC the cells own genes and preventing their expression. The polynucleotides
CC may also be used as DNA probes in diagnostic assays. The SPs may also be
CC used as antigens to produce antibodies and to identify modulators
CC (agonists and antagonists) of the SPs. The anti-(SP) antibodies and
CC antagonists may also be used to down regulate expression and activity of
CC SP and as diagnostic agents for detecting the presence of SPs in samples.
CC The disorders include for example: immune/autoimmune diseases (e.g. HIV
CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
CC and multiple sclerosis), cancers and hyperproliferative disorders (e.g.
CC melanomas, neoplasms of the breast or liver, Sezary syndrome and
CC Gaucher's disease), neurological diseases (e.g. Alzheimer's disease,
CC Parkinson's disease), cardio-/cerebrovascular disorders (e.g. cardiac
CC arrest, tachycardia and angina), infections caused by bacteria, viruses
CC and fungi and ocular disorders (e.g. corneal infections). Other uses
CC include wound healing, maintenance of organs before transplantation,
CC
Query Match 99.0%; Score 1267; DB 22; Length 246;
Best Local Similarity 99.6%; Pred. No. 1.7e-125;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 SEITVAEVRKNEKSSGINTASSAASKERTAPUKSNTGPKLACSLIFLLATISFF 62
Db 12 AEITYAEVRKNEKSSGINTASSAASKERTAPUKSNTGPKLACSLIFLLATISFF 71
QY 63 IAFYIFQKYSQLEKTKTLEKVTLECAKKNPVEERTAMSCCPKMKSSSCYFIST 122
72 IAFYIFQKYSQLEKTKTLEKVTLECAKKNPVEERTAMSCCPKMKSSSCYFIST 131
QY 123 ESASMOSEKDCARMEAHLYNTQEOEDFFQNLQESAFVGLSDPEGRRHOMWDOT 182
Db 132 ESASMOSEKDCARMEAHLYNTQEOEDFFQNLQESAFVGLSDPEGRRHOMWDOT 191
QY 183 PYNESSTFWHPRSDPNERCVLNFRRKSPKRMGMNDVNCIGPORSVCENMKIHL 237
Db 192 PYNESSTFWHPRSDPNERCVLNFRRKSPKRMGMNDVNCIGPORSVCENMKIHL 246
RESULT 7
ABP47873
ID ABP47873 standard; Protein: 246 AA.
XX
XX ABP47873;
XX
XX 23-AUG-2002 (first entry)
DE Human polypeptide SEQ ID NO 303.
XX
XX Human: nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnerrary;
KW antiparkinsonian; antistickling; antianemic; antiarthritic; cancer;
KW

KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiatic; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX US2002042386-A1.
XX
XX 11-APR-2002.
XX
XX 17-JAN-2001; 2001US-0764870.
XX
XX 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 28-JUN-2000; 2000US-214886P.
PR 07-JUL-2000; 2000US-216647P.
PR 11-JUL-2000; 2000US-216880P.
PR 11-JUL-2000; 2000US-217487P.
PR 14-JUL-2000; 2000US-217496P.
PR 26-JUL-2000; 2000US-218290P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.
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PR 22-AUG-2000; 2000US-226868P.
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PR 01-SEP-2000; 2000US-229287P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
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PR 05-SEP-2000; 2000US-229509P.
PR 05-SEP-2000; 2000US-229513P.
PR 08-SEP-2000; 2000US-231413P.
PR 21-SEP-2000; 2000US-234223P.
PR 21-SEP-2000; 2000US-234274P.
PR 25-SEP-2000; 2000US-234977P.
PR 27-SEP-2000; 2000US-235834P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236367P.
PR 29-SEP-2000; 2000US-236368P.
PR 29-SEP-2000; 2000US-236369P.
PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 02-OCT-2000; 2000US-237040P.
PR 13-OCT-2000; 2000US-239335P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241809P.
PR 01-NOV-2000; 2000US-244617P.
PR 17-NOV-2000; 2000US-249299P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.
XX
XX (ROSE/) ROSEN C A.
PA (RUBEN/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
XX Rosen CA, Ruben SM, Barash SC;
PI
XX
XX WPI; 2002-470713/50.
DR N-PSDB; ABQ65548.
XX

XX	PS	Claim 11; SEQ ID NO 303; 235pp + Sequence Listing; English.
XX	CC	The invention relates to novel genes (AB066521-AB066785) and proteins
XX	CC	(ABP47846-ABP48110) useful for preventing, treating or ameliorating
XX	CC	medical conditions e.g. by protein or gene therapy. The genes are
XX	CC	isolated from a range of human tissues disclosed in the specification.
XX	CC	The nucleic acids, proteins, antibodies and (ant)agonists are useful
XX	CC	In the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
XX	CC	and ovarian cancer and other cancers of the adrenal gland, bone, bone
XX	CC	marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
XX	CC	(b) immune disorders e.g. Addison's disease, allergies, autoimmune,
XX	CC	haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
XX	CC	disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX	CC	colitis; (c) cardiovascular disorders such as myocardial ischaemias;
XX	CC	(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
XX	CC	epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
XX	CC	and parasitic infections.
XX	CC	Note: The sequence data for this patent did not form part of the
XX	CC	printed specification, but was obtained in electronic format directly
XX	CC	from USPTO at seqdata.uspto.gov/sequence.html?docID=99909764870.
XX	SO	Sequence 246 AA:
OY	Query Match	99.0%; Score 1267; DB 23; Length 246;
OY	Best Local Similarity	99.6%; Pred. No. 1,7e-125;
Db	Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0	
OY	3 SEITTAETFRKNEFKSSGINTASSAASERTAPLKSNTGFKLDCASLIIFLLAISFF 62	
Db	12 AEITYAEVRFKNFEKSSGINTASSAASERTAPLKSNTGFKLDCASLIIFLLAISFF 71	
OY	63 IAFVTFPKYSQQLLEKTKTKELVHTTLGCYKKNMVEEPAWCCCKNNKSFSSNCFYST 122	
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Db	132 ESASWDSSEKDCARMEAHLLVINTEEDDFIFQNLDESAYFVGSLDESGORHMQWVDOT 191	
OY	183 PYNESSTFWHPREBPDNERCVVLNFERSPKRMGNNDVNCIGPQSVCEMKIHL 237	
Db	192 PYNESSTFWHPREBPDNERCVVLNFERSPKRMGNNDVNCIGPQSVCEMKIHL 246	
OS	RESULT 8	
AC	ABP63043	
ID	ABP63043 standard; Protein; 198 AA.	
XX	ABP63043;	
XX	14-OCT-2002 (first entry)	
DE	Human polypeptide seq ID NO 480.	
XX	Human; vulnetary; dermatological; neuroprotective; noctropic; cancer;	
KW	antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;	
KW	antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;	
KW	burn; central nervous system disorder; Alzheimer's disease;	
KW	Parkinson's disease; Huntington's disease; immune disorder;	
XX	autoimmune disorder; multiple sclerosis; diabetes; allergy.	
OS	Homo sapiens.	
PN	WO200218424-A2.	
XX	07-MAR-2002.	
PD	31-AUG-2001; 2001WO-US27093.	
XX		

PR	01-SEP-2000; 2000US-0654935.	
XX	(HYSE-) HYSEQ INC.	
PA		
PI	Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;	
PI	Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;	
XX		
DR	WPI: 2002-583321/62.	
XX	N-PSDB: ABO93522.	
XX		
PT	New polynucleotide and polypeptides, useful for treatment and diagnosis	
PT	of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral	
PT	sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple	
PT	sclerosis, diabetes and allergies -	
XX		
PS	Claim 20; SEQ ID NO 480; 284pp + Sequence Listing; English.	
XX		
CC	The invention relates to an isolated polynucleotide (I) comprising one of	
CC	245 sequences (ABO93288-ABO93532). Treating a condition comprising	
CC	administering to a mammalian subject a composition comprising the protein	
CC	(II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).	
CC	(I), (II) and (III) are useful for diagnostic evaluation of disorders.	
CC	(I) is useful for gene therapy of diseases and (II) can be used for	
CC	therapeutic treatment. Diseases that may be treated include wound healing	
CC	and tissue repair, burns, central nervous system disorders (e.g.	
CC	Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral	
CC	sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple	
CC	sclerosis, diabetes and allergies.	
CC	Note: The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pcl_sequences.	
XX		
SO	Sequence 198 AA;	
	Query Match 82.8%; Score 1059.5; DB 23; Length 198;	
	Best Local Similarity 83.1%; Pred. No. 1.1e-103;	
	Matches 197; Conservative 1; Mismatches 0; Indels 39; Gaps 1;	
OY	1 MTSETTYAEVRFKNEKSSGGINTAASAKERTAPLNSNGEPKLLCASLIFLLLAIS 60	
DB	1 MTSETTYAEVRFKNEKSSGGINTAASAKERTAPLNSNGEPKLLCASLIFLLLAIS 27	
OY	61 FFIAFVIEFOKYSQLLEKTKKELVHTTLECVKKNMPVEETAWSCCPKNNKSSNCFI 120	
DB	28 -----VFQKYSQLEKTKKELVHTTLECVKKNMPVEETAWSCCPKNNKSSNCFI 81	
OY	121 STESAMQDSKDCARNEAHLVINTQEDDFIQNLQESBAYVGLSDPEGQRHMOWD 180	
DB	82 STESAMQDSKDCARNEAHLVINTQEDDFIQNLQESBAYVGLSDPEGQRHMOWD 141	
OY	181 QTPNNESTFVHNPSPDNERCYVLFNFKSPKRWGNDVNCILPQNSVCEMAKTHL 237	
DB	142 QTPNNESTFVHNPSPDNERCYVLFNFKSPKRWGNDVNCILPQNSVCEMAKTHL 198	
RESULT 9		
ID	AAW88128 standard; Protein: 238 AA.	
XX	AAW88128;	
AC		
XX	11-MAY-1999 (first entry)	
DT		
XX	Rodent DCMPI C-I lectin family gene protein sequence.	
XX		
XX	Rodent dendritic cell membrane protein; DCMPI; DCMPI2;	
XX	chromosomal abnormality; expression misregulation;	
XX	abnormal proliferation; regeneration; degeneration; haematopoietic cell.	
OS	Mammalia.	
XX		
XX	W09902562-A1	

PD 21-JAN-1999.
 XX 08-JUL-1998; 98WO-US13436.
 PF 09-JUL-1997; 97US-0053080.
 PR (SCHE) SCHERING CORP.
 XX Bates EEM, Ford J, Lebecque SJE, Ravel O, Saeland S;
 PI Valladeau J;
 DR WPI: 1999-120786/10.
 N-PSDB; AAX04867.
 XX Dendritic cell membrane proteins - used to treat conditions
 PT associated with abnormal physiology or development
 XX Claim 1; Page 73-75; 82pp; English.
 PS Dendritic cell membrane protein 1 (DCMP1) and DCMP2 nucleic acids can be
 CC used as markers for distinguishing cell types, including genomic aspects
 CC of cells, as well as mRNA and protein expression patterns. They can also
 CC be used to detect chromosomal abnormalities. The proteins can be used to
 CC diagnose disorders associated with expression misregulation. They can
 CC also be used to treat conditions associated with abnormal physiology or
 CC development, including abnormal proliferation, e.g. cancerous conditions
 CC or degenerative conditions. Abnormal proliferation, regeneration,
 CC degeneration and atrophy may be modulated using the proteins. The
 CC proteins may also play a role in regulation or development of
 CC haematopoietic cells.
 CC
 CC Sequence 238 AA;
 SO
 Query Match 52.5%; Score 672.5; DB 20; Length 238;
 Best Local Similarity 53.3%; Pred. No. 1.3e-62;
 Matches 129; Conservative 37; Mismatches 67; Indels 9; Gaps 6;
 OY 1 MTSETTYAENVKKEFKSSGINTASSAASKERTAPLKS--NTGFPKLCASLIFELLILA 58
 DB 1 MASETTYAEVAKFNE--SNSLHTYSESPAAREKPIRLKRPQSGSLITSLMLLLILA 58
 OY 59 ISFTIAVIEFQKYSQLL-EKKTKELVHTTLECVKKNMPYETAWSCCPKRWKSSSNC 117
 DB 59 ITFLVAFITIFQKYSQLL-EKKTKELVHTTLECVKKNMPYETAWSCCPKRWKSSSNC 118
 OY 118 YFIST--ESASWQSEKDCARMEHLVYINQEQDFTFQNLQESAFVGLSPDEGRH 175
 DB 119 YLVPVSSASWMSSEKSCRMGAHLVYIOEQDFTTGLDTHAAVFIQLMD-TGHRQ 177
 OY 176 WQWVDQPFYNESTFMHREPSDNERCVLNFKSPKRWGMNDVNCGPQSVCEMKKI 235
 DB 178 WQWVDQPFYNESTFMHREPSDNERCVLNFKSPKRWGMNDVNCGPQSVCEMKKI 236
 OY 236 HL 237
 DB 237 NL 238
 RESULT 10
 AAEL2080 standard; Protein; 211 AA.
 ID AAEL2080 standard; Protein; 211 AA.
 AC AAEL2080;
 XX
 XX 18-DEC-2001 (first entry)
 DE Dendritic cell (DC) DCEC/SPLICE 1 variant protein.
 XX
 XX Dendritic cell; DC; DCEC protein; gene therapy; dermatological; vaccine;
 KW atopic dermatitis; autoimmune disease; inflammatory skin disease; cancer;
 KW immunosuppressive; AIDS; Acquired immune deficiency syndrome; cytostatic;
 KW chromosomal identification; pharmaceutical; hypersensitivity; virucide;
 KW transplant rejection; chronic inflammatory disease; anti-HIV; variant.

XX Unidentified.
 OS Location/Qualifiers
 XX Key
 FH Misc-difference 1
 FT /note= "Encoded by C"
 PN MO20012773-A2.
 PD 04-OCT-2001.
 XX 28-MAR-2001; 2001WO-EP03542.
 PF 29-MAR-2000; 2000US-192934P.
 PR 18-MAY-2000; 2000US-205020P.
 PR 18-MAY-2000; 2000US-205026P.
 PR 19-MAY-2000; 2000US-205767P.
 PR 19-MAY-2000; 2000US-205769P.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 PI Werner G, Phares W, Jaritz W, Lapp H, Kalthoff FS;
 DR WPI: 2001-616466/71.
 N-PSDB; AAD19730.
 XX New polypeptides for screening therapeutic agonists and antagonists
 PT comprise dendritic cell polypeptides -
 XX
 PS Claim 2; Page 52; 52pp; English.
 CC The invention relates to dendritic cell (DC) proteins and their
 CC corresponding DNA molecules. A pharmaceutical composition comprising
 CC agonist and antagonist of DC proteins are useful for treating abnormal
 CC conditions related to both an excess of and insufficient level of
 CC expression of DC gene, or related to both an excess of and insufficient
 CC activity of DC protein. Soluble form of DC proteins are used as an active
 CC ingredient in combination with pharmaceutical acceptable carriers.
 CC DC genes and proteins are useful for treating chronic inflammatory
 CC diseases, autoimmune diseases, transplant rejection crisis, including
 CC inflammatory skin diseases such as contact hypersensitivity, atopic
 CC dermatitis or virally-induced immune suppression such as AIDS and cancer.
 CC DC protein is useful for inducing immunological response in a mammal, and
 CC as immunogen to produce antibodies immunospecific for the polypeptide.
 CC DC gene is useful in gene therapy. DC gene is also useful as a diagnostic
 CC reagent, and for chromosomal identification. The present sequence is
 CC dendritic cell (DC) DCEC/SPLICE 1 variant protein which is found to
 CC belong to the family of C-type lectins with one single carbohydrate
 CC recognition domain at the C-terminal end.
 CC
 CC Sequence 211 AA;
 SO
 Query Match 43.1%; Score 552; DB 22; Length 211;
 Best Local Similarity 47.7%; Pred. No. 6.1e-50;
 Matches 102; Conservative 42; Mismatches 60; Indels 10; Gaps 4;
 OY 28 ASKERTAPLKSNTGFPKLCASLIFELLILAISFTIAVY----FQKYSQLEKKTKE 83
 DB 4 ASEDRE--KGLMFWOLKWSMAYVSTLLSVCFVSSVPHNEMYSTVRLSKLREYQ 60
 OY 84 LVHTTLECVKKNMPYETAWSCCPKRWKSSSNCYFISTESASWQSEKDCARMEHLV 143
 DB 61 QYHPSLITVCMGCKDIED--WSCCPRTWTSFSSCTFISTGMSWTKSKNCSYMGADLV 118
 OY 144 INTQEQDFTFQNLQESAFVGLSPDEGRHMQWVDQPFYNESTFMHREPSDNERC 203
 DB 119 INTRREQDFTFQNLKRNSSYFLGLSDPGGRHMQWVDQPFYNEVTFWHSCEPNLIDERC 178
 OY 204 VLVNFRKSPKRWGMNDVNCGLPQSVCEMKKIHL 237
 DB 179 AINFRSS-EDMGWMDHCHVPOKSIKMKKIYI 211

RESULT 11
ID AAB84215 standard; Protein: 213 AA.
AC AAB84215;
XX 06-AUG-2001 (first entry)
XX
XX Amino acid sequence of BDCA-2 antigen isoform.
DE
XX BDCA-2; hematopoietic cell; dendritic cell; BDCA-3; BDCA-4;
KM viral infection; autoimmune disease; allergic response; cancer.
XX
XX Homo sapiens.
XX WO200136487-A2.
XX PN 25-MAY-2001.
XX
XX 15-NOV-2000; 2000MO-IB01832.
XX
XX 15-NOV-1999; 99US-0165555.
PR 23-NOV-1999; 99US-0167076.
PR 28-JAN-2000; 2000US-0179003.
PR 07-FEB-2000; 2000US-0180775.
PR 11-APR-2000; 2000US-0196824.
PR 13-APR-2000; 2000US-0197205.
XX
XX (MILT-) MILTENYI BIOTECH GMBH.
XX PI Schmitz J, Dzionek A, Buck DW;
XX
XX WPI: 2001-355622/37.
DR N-PSDB; AAF90241.
XX
XX Compositions and cell populations enriched in dendritic cells through
PT use of antigen-binding fragments specific for BDCA-2, BDCA-3 or
PT BDCA-4, are used to treat viral infections, autoimmune diseases,
PT allergic responses and cancer.
XX
XX Claim 122; Fig 5; 115pp; English.
XX
XX The present sequence represents an antigen designated BDCA-2. The
CC specification describes compositions and hematopoietic cell populations
CC enriched in dendritic cells (DCs). These compositions are produced using
CC antigen-binding fragments specific for BDCA-2, BDCA-3 or BDCA-4. The DCs
CC obtained are used to treat viral infections, autoimmune disease, allergic
CC response, and cancer. BDCA-1, BDCA-2, BDCA-3 and BDCA-4 monoclonal
CC antibodies and their antigen-binding fragments are used to detect,
CC enumerate and isolate DC populations from leukapheresis material, whole
CC blood and tonsils and from non-hematopoietic and hematopoietic tissues.
XX
XX
SQ Sequence 213 AA:
Query Match 43.1%; Score 551.5; DB 22; Length 213;
Best Local Similarity 50.8%; Pred. No. 7e-50;
Matches 97; Conservative 38; Mismatches 49; Indels 7; Gaps 3;
QY 51 LIFLLAIISFFIAFYI---FQKYSQLEKTKTKELVHTTLECKKKNPVETAMSCC 106
DB 26 VASILLISVCFYSSVPHNFMYSKYVKRLSKLREYQOYHPSLTCWEGKDID--WSCC 83
QY 107 PKMKSPSSNCYIFSTESASMODEKDCARMEAHLLVINTQEOODFIQNLQESAYFVG 166
DB 84 PTPWTSFQSSCYRISTGMSQWTSQKNCSTMGADLVYINTREODPIQNLKRNSTFTLG 143
QY 167 LSDPEQRHQMWDQTPYNNSTFWHPREPSDNERCVVNLNFKSPKRMGMNDVNCIGPQ 226
DB 144 LSDPGGRHQMWDQTPYNNSTFWHPREPSDNERCVVNLNFKSPKRMGMNDVNCIGPQ 226
QY 227 RSYCEMKKIHL 237
DB 227 RSYCEMKKIHL 237

DB 203 KSICKMKKIYI 213
RESULT 12
ID AAE27987 standard; Protein: 213 AA.
AC AAE27987;
XX 27-JAN-2003 (first entry)
XX
XX Human dectin protein #1.
DE
XX Human; dectin; novel human protein; NHP; gene therapy; cancer; arthritis;
KM inflammatory disorder; infection; cytostatic; antibacterial.
XX
XX Homo sapiens.
XX WO200272603-A2.
XX PN 19-SEP-2002.
XX
XX 01-MAR-2002; 2002MO-US06711.
PR 12-MAR-2001; 2001US-274961P.
PR
XX (LEXI-) LEXICON GENETICS INC.
XX PA Turner CA, Mathur B, Cullinan EB;
XX PI
XX WPI: 2002-723313/78.
DR N-PSDB; AAD46320.
XX
XX New isolated NHP nucleic acid molecule, useful for diagnosing and/or
PT treating disorders associated with aberrant NHP expression and
PT activity, such as cancer, inflammatory disorders, arthritis and
PT infection.
XX
XX Claim 2; Page 35-36; 37pp; English.
XX
XX The present sequence is dectin protein, a novel human protein
CC (NHP). NHP sequences are used in gene therapy. They can also be used
CC as hybridisation probes for screening libraries. The compositions and
CC methods of the present invention are useful for diagnosing and/or
CC treating disorders associated with aberrant NHP expression and activity,
CC such as cancer, inflammatory disorders, arthritis and infection.
XX
XX
SQ Sequence 213 AA:
Query Match 43.1%; Score 551.5; DB 23; Length 213;
Best Local Similarity 50.8%; Pred. No. 7e-50;
Matches 97; Conservative 38; Mismatches 49; Indels 7; Gaps 3;
QY 51 LIFLLAIISFFIAFYI---FQKYSQLEKTKTKELVHTTLECKKKNPVETAMSCC 106
DB 26 VASILLISVCFYSSVPHNFMYSKYVKRLSKLREYQOYHPSLTCWEGKDID--WSCC 83
QY 107 PKMKSPSSNCYIFSTESASMODEKDCARMEAHLLVINTQEOODFIQNLQESAYFVG 166
DB 84 PTPWTSFQSSCYRISTGMSQWTSQKNCSTMGADLVYINTREODPIQNLKRNSTFTLG 143
QY 167 LSDPEQRHQMWDQTPYNNSTFWHPREPSDNERCVVNLNFKSPKRMGMNDVNCIGPQ 226
DB 144 LSDPGGRHQMWDQTPYNNSTFWHPREPSDNERCVVNLNFKSPKRMGMNDVNCIGPQ 202
QY 227 RSYCEMKKIHL 237
DB 203 KSICKMKKIYI 213
RESULT 13
ID AAE12079 standard; Protein: 218 AA.

XX	AAE12079;	
AC		
XX		
XX	18-DEC-2001	(first entry)
DT		
XX		
DE	Dendritic cell (DC)	DCLEC protein.
XX		
KW	Dendritic cell; DC; DCLEC protein; gene therapy; dermatological; vaccine;	
KW	atopic dermatitis; autoimmune disease; inflammatory skin disease; cancer;	
KW	immunosuppressive; AIDS; Acquired immune deficiency syndrome; cytostatic;	
KW	chromosomal identification; pharmaceutical; hypersensitivity; virucide;	
KW	transplant rejection; chronic inflammatory disease; anti-HIV.	
XX		
OS	Unidentified.	
XX		
Key		
FH	Location/Qualifiers	
FT	26..46	
FT	/note= "Single transmembrane region"	
FT	114..211	
FT	/note= "Extracellular C-type lectin domain"	
XX		

04-OCT-2001.

28-MAR-2001; 2001WO-EP03542.

XX 29-MAR-2000; 2000US-192934P
PR 18-MAY-2000; 2000US-205020P
PR 18-MAY-2000; 2000US-205026P
PR 19-MAY-2000; 2000US-205767P
PR 19-MAY-2000; 2000US-205769P

PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH

PI. Werner G, Phares W, Jaritz M, Lapp H, Kalthoff FS;

DR WPI; 2001-616466/71.
DR N-PSDB; AAD19729.

PT New polypeptides for screening therapeutic agonists and antagonists
PT comprise dendritic cell polypeptides -
XX
PS Claim 2, Page 51, 52pp; English.

CC The invention relates to dendritic cell (DC) proteins and their
CC corresponding DNA molecules. A pharmaceutical composition comprising
CC agonist and antagonist of DC proteins are useful for treating abnormal
CC conditions related to both an excess of and insufficient level of
CC expression of DC gene, or related to both an excess of and insufficient
CC activity of DC protein. Soluble form of DC proteins are used as an active
CC ingredient in combination with pharmaceutical acceptable carriers.
CC DC genes and proteins are useful for treating chronic inflammatory
CC diseases, autoimmune diseases, transplant rejection crisis, including
CC inflammatory skin diseases such as contact hypersensitivity, atopic
CC dermatitis or virally-induced immune suppression such as AIDS and cancer.
CC DC protein is useful for inducing immune suppression in a mammal, and
CC as immunogen to produce antibodies immunospecific for the polypeptide.
CC DC gene is useful in gene therapy. DC gene is also useful as a diagnostic
CC reagent, and for chromosomal identification. The present sequence is
CC dendritic cell (DC) DCLE protein identification. It is found to belong to the family
CC of C-type lectins with one single carbohydrate recognition domain at the
CC C-terminal end.

sq Sequence 218 AA;

Query Match 43.18; Score 551.5; DB 22; Length 218;

Matches 97; Conservative 38; Mismatches 49; Indels 7; Gaps 3;

```

51 LIFELLALSFIAFVI----FQKXSQLEKKTTELVTHTTECKAKNMPYEETAMSCC 106
:: ||:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |::

```

Db	3	VSEILLLSVCFYSSSVVPHNFMYSKTVKRLSLRREYQYHPSLCLVMEGRKIED--	-NSCC	88
QY	107	PKMKSFSSNCYETISTESASQDSEKDCARMEAHLLVINTQEBODFTIQTQESAYFVG		166
Db	89	PTFWTSFQSSCYFISTGMQSWTKRSQKNCVMACADLVVINTFREEDPFIQNLKRRSSYFLG		148
QY	167	LSDPGGRHQHWQDQTFPYNESSTFWHLRPPSPDNRRCVYLVNFKRSPKRWGANDVNCGLPQ		228
Db	149	LSDPGGRHQHWQDQTFPYNEENVTFWHSGEPPNLLDERCALINFRSS-EEGWANDHICHVPQ		207
QY	227	RSVCEMKKTIHL	237	
Db	208	KSIICKMKKIYI	218	

RESULT 1.4

ID AAE27988 standard; Protein; 182 AA.

AC AAE27988;

DT 27-JAN-2003 (first entry)

Human dectin protein #2.

KW Human; dectin; novel human protein; NHP; gene therapy; cancer; arthritis;

[illegible]XX
XX
XX

FT Misc-difference, 35

Encoded by YCA"

PN WO200272603-A2

PD. 19-SEP-2002

PF 01-MAR-2002; 2002WO-US06711.
xy

PR 12-MAR-2001; 2001US-274961P.

PA (LEXI-) LEXICON GENETICS INC.

PI Turner CA, Mathur B, Cullinan EB;
v

DR WPI; 2002-723313/78.

[illegible]

PT treating disorders associated with aberrant NHP expression and activity such as cancer, inflammatory disorders, arthritis and DM

PT infection -

PS Claim 4; Page 36-37; 37pp; English.
xx

CC The present sequence is dectln protein, a novel human protein
CC (NHP) NHP sequences are used in gene therapy. They can also

CC as hybridisation probes for screening libraries. The compositions and methods of the present invention are useful for diagnosing and/or

CC treating disorders associated with aberrant NHP expression and activity,
CC such as cancer, inflammatory disorders, arthritis and infection

XX	Sequence	182 AA:
SC		

Query Match

Best Local Similarity 54.4%; Pred. NO. 3.6e-48;
Matches 92: Conservative 31: Mismatches 43: Indels 3: Gaps 2:

69 FOKYSOI.I.EKKTTKEI.VHTTI.ECVKK.NBPVEET.AWSCC.BK.NK.SSS.NCYETSTESAS.WO 128

Db 17 YSKTVKRI.SKI.REYNOYHYST.TCYMECKDIED--WSCCPBPWTSEOSSCYETSTCMOSWT 7A

OY 129 DSEKDCARMEAHLLVINTQEEODFIQNLQESAYFGLSDPEGGRHQMOWDQTPYNESS 188
 DB 75 KSKKNCYWGADLVYINTREEDFIQNLKRNSYFGLSDPEGGRHQMOWDQTPYNNV 134
 OY 189 TFWHRESDNERECVYNFRKSPKRWGNDVNCIGPDRSCVEMKKIHL 237
 DB 135 TFWHSGEPNNLDERCAIINFRRS-BEWMNDIHCHVPOKSIKMKKIYI 182

RESULT 15
 AAU98013
 ID AAU98013 standard; Protein; 134 AA.
 AC AAU98013;
 XX
 DT 27-AUG-2002 (first entry)
 XX

Human partial dendritic cell immunoreceptor #1.

KW Human; dendritic cell immunoreceptor; cytosolic;
 KW antihistaminic; anorectic; antidiabetic; cancer; allergy; anaphylaxis;
 KW asthma; inflammation; obesity; diabetes; central nervous system disorder;
 KW Alzheimer's disease; Parkinson's disease; dementia; osteoarthritis;
 KW cardiovascular disorder; myocardial infarction; ischaemic heart disease;
 KW congestive heart failure; chronic obstructive pulmonary disease; COPD.
 XX
 OS Homo sapiens.
 XX
 PN MO200232958-A2.
 PD 25-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-EP11812.
 XX
 PR 16-OCT-2000; 2000US-240096P.
 PR 27-AUG-2001; 2001US-314661P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Smolyar A;
 XX
 DR WPI: 2002-463308/49.
 DR N-PSDB; ARK52903.
 XX

Novel human dendritic cell immunoreceptor polypeptide, useful for treating cancer, asthma, obesity, diabetes, central nervous system disorder or cardiovascular disorder

Claim 25; Fig 2; 114pp; English.

The invention relates to a purified human dendritic cell immunoreceptor polypeptide and its encoding nucleic acid. Also included are an expression vector comprising the nucleic acid, a host cell containing the vector, reducing the activity of human dendritic cell immunoreceptor involves contacting a cell with a reagent which specifically binds to the polypeptide or nucleic acid and a reagent that modulates the activity of the polypeptide or nucleic acid. The reagent is useful for the preparation of a medicament for modulating the activity of human dendritic cell immunoreceptor in a disease such as cancer, allergy, anaphylaxis, asthma, inflammation, obesity, diabetes, a central nervous system (CNS) disorder (e.g. Alzheimer's disease, Parkinson's disease or dementia), or a cardiovascular disorder (e.g. myocardial infarction, ischaemic heart disease, congestive heart failure), chronic obstructive pulmonary disease (COPD) and osteoarthritis (many other diseases and disorders are listed in the specification). The polypeptide and nucleic acid are useful for identifying test compounds which act as agonists or antagonists, for raising specific antibodies, and as a bait protein in a two-hybrid or three-hybrid assay. The nucleic acid is useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to disease and abnormalities related to the presence of mutations. The present sequence represents a partial sequence of a dendritic cell immunoreceptor.

XX
 SQ Sequence 134 AA;
 Query Match 39.6%; Score 507.5; DB 23; Length 134;
 Best Local Similarity 62.2%; Pred. No. 1.7e-45;
 Matches 84; Conservative 24; Mismatches 26; Indels 1; Gaps 1;

OY 103 WSCCPKNNKSFSSNCFYFISTESASWQSEKDCARMEAHLLVINTQEEODFIQNLQESYA 162
 DB 1 MSCCPTPMTSPFSSCYFISTGMSWTKGKNCYWGADLVYINTREEDFIQNLKRNS 60
 OY 163 YFVGLSDPEGGRHQMOWDQTPYNESSFTWHPRESDNERECVYNFRKSPKRWGNDVNC 222
 DB 61 YFGLSDPEGGRHQMOWDQTPYNNVTFWHSGEPPNNLDERCAIINFRRS-BEWMNDIHCH 119
 OY 223 LGPDRSCVEMKKIHL 237
 DB 120 HYPKSIKMKKIYI 134

Search completed: August 4, 2003, 13:08:38
 Job time : 87 secs

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OM protein - protein search, using sw model

Run on: August 4, 2003, 13:07:18 ; Search time 30 Seconds

(without alignments)
334.256 Million cell updates/sec

Title: US-09-862-802-2

Perfect score: 1280
Sequence: 1 MTSEITYAEFRFKNEKSSG.....NDVNCGLGPRQVCEMKIHL 237

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

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- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCBUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1280	100.0	237	3	US-09-111-470-2
2	672.5	52.5	238	3	US-09-111-470-8
3	489	38.2	209	3	US-08-772-440-4
4	473.5	37.0	167	3	US-08-772-440-21
5	452.5	35.4	145	3	US-08-772-440-14
6	452.5	35.4	175	3	US-08-772-440-15
7	427.5	33.4	131	3	US-08-772-440-23
8	427.5	33.4	131	3	US-08-772-440-27
9	330.5	25.8	168	3	US-08-772-440-17
10	325	25.4	134	3	US-08-772-440-16
11	277.5	21.7	149	4	US-09-489-847-167
12	256.5	20.0	273	3	US-09-111-470-10
13	256.5	20.0	292	2	US-08-688-342-4
14	256.5	20.0	292	2	US-09-113-788-4
15	253	19.8	316	3	US-09-111-470-4
16	240	18.8	85	3	US-08-772-440-32
17	238	18.6	87	4	US-09-489-847-326
18	226	17.7	287	4	US-09-111-470-6
19	220.5	17.2	291	2	US-08-688-342-5
20	220.5	17.2	291	2	US-09-113-788-5
21	220.5	17.2	291	3	US-09-111-470-5
22	218.5	17.1	75	3	US-09-111-470-11
23	212.5	16.6	129	3	US-08-722-126A-10
24	212.5	16.6	129	3	PCT-US95-04258-10
25	210	16.4	272	1	US-08-690-095-1
26	210	16.4	272	3	US-09-113-789-1
27	208.5	16.3	287	1	US-08-365-103B-4

28	208.5	16.3	300	1	US-08-365-103B-6	Sequence 6, Appl
29	208.5	16.3	327	1	US-08-365-103B-2	Sequence 2, Appl
30	207	16.2	1479	3	US-08-840-062-2	Sequence 2, Appl
31	205.5	16.1	404	4	US-09-517-605-2	Sequence 2, Appl
32	204	15.9	1479	3	US-08-840-062-4	Sequence 4, Appl
33	196.5	15.4	125	3	US-08-722-126A-7	Sequence 7, Appl
34	196.5	15.4	125	5	PCT-US95-04258-7	Sequence 7, Appl
35	192.5	15.0	187	4	US-09-535-521-17	Sequence 17, Appl
36	192.5	15.0	208	4	US-09-535-521-20	Sequence 20, Appl
37	192.5	15.0	292	4	US-09-535-521-2	Sequence 2, Appl
38	192.5	15.0	292	4	US-09-535-521-5	Sequence 5, Appl
39	192	15.0	111	6	5514582-11	Patent No. 5514582
40	191	14.9	190	4	US-09-127-946-14	Sequence 14, Appl
41	190	14.8	280	4	US-09-986-243-119	Sequence 319, App
42	188	14.7	123	4	US-09-535-521-25	Sequence 25, Appl
43	188	14.7	128	4	US-09-535-521-8	Sequence 8, Appl
44	188	14.7	139	4	US-09-535-521-11	Sequence 11, Appl
45	188	14.7	141	4	US-09-535-521-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-111-470-2
Sequence 2, Application US/09111470
Patent No. 627959

GENERAL INFORMATION:
APPLICANT: Valladeau, Jenny
APPLICANT: Ravel, Odile
APPLICANT: Bates, Elizabeth E.M.
APPLICANT: Ford, John
APPLICANT: Saeland, Sem
APPLICANT: Lebeque, Serge J.E.
TITLE OF INVENTION: Mammalian Membrane Protein Genes;
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,470
FILING DATE: 08-JUL-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,080
FILING DATE: 09-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: SF0695
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-111-470-2

Query Match 100.0%; Score 1280; DB 3; Length 237;
Best Local Similarity 100.0%; Pred. No. 6.1e-137;

	Matches	237	Conservative	0	Mismatches	0	Indels	0	Gaps	0
Qy	1	MTSETTAAEAVFKNPKNEFKSSGINTASSAASKERTATLKSNTGPKPLCLASLIFELLILAIS	60							
Db	1	MTSETTAAEAVFKNPKNEFKSSGINTASSAASKERTATLKSNTGPKPLCLASLIFELLILAIS	60							
Qy	61	FFIAFVIEFFQKYSOLLEKKTRELVTHTLECYKKMMPVETRMWSCCPKMKKSFSSNCFYI	120							
Db	61	FFIAFVIEFFQKYSOLLEKKTRELVTHTLECYKKMMPVETRMWSCCPKMKKSFSSNCFI	120							
Qy	121	STESASWDSKDCARMEAHLLVINTQEODFIFONLOEBSAYFVGLSDPEGQRHMOWD	180							
Db	121	STESASWDSKDCARMEAHLLVINTQEODFIFONLOEBSAYFVGLSDPEGQRHMOWD	180							
Qy	181	QTPYNESSTFWHPRPSPDPNRCVYLNFRKSPKRGKMDVNLGQORSVCEMMKTHL	237							
Db	181	QTPYNESSTFWHPRPSPDPNRCVYLNFRKSPKRGKMDVNLGQORSVCEMMKTHL	237							

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Db      1 MASEITIAAVKFRKNE--SNSLHTYSESPAAPREKPIRDLRKPGSPILTLISMLLTLA 58
QY      59 ISFFIAFVIFPQKYSQL-EKKTTELHYHTLIECYKKMMPYEELTANSCCPRNKSSSNC 117
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      59 ITFLVAFIIFYFKYSQLEEKRAAKRNIMHNELNCTKSVSPEDKWCSCPRDMLTFSHC 118
QY      118 YFIST--ESASODSEKDCARMEAHLLVINTQOEODFIQOMIOEESAFVGLSDPEGORH 175
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Db      119 YLVPITYSSASNNKSSENCNRGALHLYIQOSEBDFITGLDTHAAYFGLMD--TGRHQ 177
QY      176 WQWVDQTPYNESSTEHMPREPSDPRRCVLTFFKSKPRKMGANDVNCIGPORSYCEMKKI 235
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      178 WQWVDQTPYEESTITFEHNGEPPSGNGEKATIIYRWK--TGQMGNDISCLRKQSVCKMKKI 236
QY      236 HL 237
Db      237 NL 238

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ULT 2
 09-111-470-8
 Sequence 8, Application US/09111470
 Patent No. 6277959
 GENERAL INFORMATION:
 APPLICANT: Valladeau, Jenny
 APPLICANT: Ravel, Odile
 APPLICANT: Bates, Elizabeth E.M.
 APPLICANT: Ford, John
 APPLICANT: Saeland, Sem
 APPLICANT: Lebecque, Serge J.E.
 TITLE OF INVENTION: Mammalian Membrane Protein Genes;
 TITLE OF INVENTION: Related Reagents
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/111,470
 FILING DATE: 08-JUL-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/053,080
 FILING DATE: 09-JUL-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: SP0695
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)852-9196
 TELEFAX: (650)496-1200
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 238 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 OS-09-111-470-8

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RESULT 3  
US-08-772-440-4  
; Sequence 4, Application US/08772440  
; Patent No. 6046158  
GENERAL INFORMATION:  
APPLICANT: ARIIZUMI, Kiyoshi  
APPICANT: Takashima, Akira  
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE  
TITLE OF INVENTION: LECTIN, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USE  
TITTLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
City: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUETER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/772,440  
FILING DATE: CONCURRENTLY HEREWITH  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTMD:493  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 209 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear
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Query Match      52.5%; Score 672.5; DB 3; length 238;
Best Local Similarity 53.3%; Pred. NO. 4.8e-68;
Matches 129; Conservative 37; Mismatches 67; Indels 9; Gaps 6;

OY      1 MTSETTAVVFPKNEFKSSGINTASSAKREKTAPLKS--NMGPKILCASLIIFPLLA 58
| | | | | | | | | | | | | : :: : : | | :: | | | | | | | | | |

```

Db 18 LMSAAIISULLSTCIASCVTYTFINDQSRRIYELHT---YHSLUCFSGGTWSE 73

QY 101 TAWSCCPKMWKFSSNCFYISTESAWODSEKDCAREAHLLVINTQEEDFTFQNLQEE 160
||| :||| :||| ||| : |||::|||::|||::|||::|||
74 KMMGCCPNHMKSPFGSSCYLISTKEHFMTSDQNCCYGAAHLVIVINTEADQNLTQOLNES 133

Dd

;; CURRENT APPLICATION NUMBER: US/09/489,847
;; CURRENT FILING DATE: 2000-01-24
;; EARLIER APPLICATION NUMBER: PCT/US99/71130
;; EARLIER FILING DATE: 1999-07-29
;; EARLIER APPLICATION NUMBER: 60/094,657
;; EARLIER FILING DATE: 1998-07-30
;; EARLIER APPLICATION NUMBER: 60/095,486
;; EARLIER FILING DATE: 1998-08-05
;; EARLIER APPLICATION NUMBER: 60/096,319
;; EARLIER FILING DATE: 1998-08-12
;; EARLIER APPLICATION NUMBER: 60/095,454
;; EARLIER FILING DATE: 1998-08-06
;; EARLIER APPLICATION NUMBER: 60/095,455
;; EARLIER FILING DATE: 1998-08-06
;; NUMBER OF SEQ ID NOS: 376
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 167
;; LENGTH: 149
;; TYPE: PRT
;; ORGANISM: Homo sapiens
S-09-489-847-167
Query Match 21.7%; Score 277.5; DB 4; Length 149;
Best Local Similarity 35.2%; Pred. No. 1.5e-23;
Matches 50; Conservative 37; Mismatches 50; Indels 5; Gaps 3;
QY 43 PRLICSL-LIFELLALISFIFVIFPQYSQLEKTKELY-HTTLCYKKNPV-- 98
D 3 POLIPSVIAVETILLGVCTFASCLVTHNPSRCKRGTVGKHLHAKKLCIKRKSLS 62
QY 99 -EEAWSCCPKRNKSFSSNCYFISTESASMODSKDCAKRAHLVINTQEDDFITQNL 157
D 63 AEGSTWACCPIDWAFQSNCFYPLTDNKTWASERNCSGGAHLMTISTAEQNFIIQFL 122
QY 158 QEESAYFVGLSDPEGQRHQMOW 179
D 123 DRRLSYFLGIDENAKGMQRMV 144
RESULT 12
US-09-111-470-10
; Sequence 10, Application US/09111470
; Patent No. 6277959
; GENERAL INFORMATION:
; APPLICANT: Valladeau, Jenny
; APPLICANT: Ravel, Odile
; APPLICANT: Bates, Elizabeth E.M.
; APPLICANT: Ford, John
; APPLICANT: Saeland, Sem
; TITLE OF INVENTION: Mammalian Membrane Protein Genes;
; TITLE OF INVENTION: Related Reagents
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,470
; FILING DATE: 08-JUL-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,080
; FILING DATE: 09-JUL-1997
; ATTORNEY/AGENT INFORMATION:

;; NAME: Ching, Edwin P.
;; REGISTRATION NUMBER: 34,090
;; REFERENCE/DOCKET NUMBER: SF0695
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650)852-9196
;; TELEFAX: (650)496-1200
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 273 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-111-470-10
Query Match 20.0%; Score 256.5; DB 3; Length 273;
Best Local Similarity 36.6%; Pred. No. 8.9e-21;
Matches 63; Conservative 25; Mismatches 63; Indels 21; Gaps 8;
QY 72 YSQL--EKKTKELYHTTLCYKKNPV--TAMSCCPKRNKSFSSNCYFISTESASW 127
D 100 HSEMLTRVQQLVDLKLTCQVATLNNNGEASTEGTCPPVNVWEHODSCYFSSGMSW 159
QY 128 QDESKDCAKRAHLVINTQEDDFITQNLQESAY-FVGLSDPEGQRHQMOWDQRPYNE 186
D 160 AEAKTYQLKNAHLVINSREQNFYQYV--GSAITWGLSDPEGA--WKWVDGTDYAT 215
QY 187 SSTFWHREPSD-----PNERCVLNFRRKSPKRMGMNDVNCIGPORSYCE 231
D 216 GFQWNRKGPDDMDGCHGLGGEDCA--HFHPDGR--WNDDVQGRPYHWCE 262
RESULT 13
US-08-688-342-4
; Sequence 4, Application US/08688342
; Patent No. 5871964
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goll, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Inocyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,342
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 292 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: Genbank

CLONE: 1235724
US-08-688-342-4

Query Match 20.0%; Score 256.5; DB 2; Length 292;
Best Local Similarity 36.6%; Pred. No. 9.8e-21;
Matches 63; Conservative 25; Mismatches 63; Indels 21; Gaps 8;

QY 72 YSQL--EKKTKELVHTTECVKKNMPVEE--TAWSCCPKMKSFSSNCYFISTESASW 127
DB 119 HSEMLLRVQQLVQDLKLTCTQVATLNNNGEASTEGTCPCPVNVWEHODSCYWFSGMSW 178
QY 128 QDSKDCARMAHLVINTQEOEPIFONLOEESAY-FVGLSDPEGORHMQWVOTPYNE 186
DB 179 AEAKEYQQLKNAHLVINSREQNFVQKYL--GSAYTWMGLSDEGA--WKWVGDTYAT 234
QY 187 SSTFMHREPSD-----PNERCVLNFRRKSPRGMNDVNCIGPORSYCE 231
DB 235 GFQWKKRGPDDMOGHGLGGGEDCA--HFHEDGR---WMDVCCORPYHWCE 281

RESULT 14

Sequence 4, Application US/09113788
Patent No. 5969104

GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,788
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/688,342
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1235724
US-09-113-788-4

Query Match 20.0%; Score 256.5; DB 2; Length 292;
Best Local Similarity 36.6%; Pred. No. 9.8e-21;
Matches 63; Conservative 25; Mismatches 63; Indels 21; Gaps 8;

QY 72 YSQL--EKKTKELVHTTECVKKNMPVEE--TAWSCCPKMKSFSSNCYFISTESASW 127

DB 119 HSEMLLRVQQLVQDLKLTCTQVATLNNNGEASTEGTCPCPVNVWEHODSCYWFSGMSW 178
QY 128 QDSKDCARMAHLVINTQEOEPIFONLOEESAY-FVGLSDPEGORHMQWVOTPYNE 186
DB 179 AEAKEYQQLKNAHLVINSREQNFVQKYL--GSAYTWMGLSDEGA--WKWVGDTYAT 234
QY 187 SSTFMHREPSD-----PNERCVLNFRRKSPRGMNDVNCIGPORSYCE 231
DB 235 GFQWKKRGPDDMOGHGLGGGEDCA--HFHEDGR---WMDVCCORPYHWCE 281

RESULT 15

Sequence 4, Application US/09111470
Patent No. 627959

GENERAL INFORMATION:
APPLICANT: Valladeau, Jenny
APPLICANT: Ravel, Odile
APPLICANT: Bates, Elizabeth E.M.
APPLICANT: Ford, John
APPLICANT: Saeland, Sem
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Membrane Protein Genes;
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,470
FILING DATE: 08-JUL-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,080
FILING DATE: 09-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: SF0695
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-111-470-4

Query Match 19.8%; Score 253; DB 3; Length 316;
Best Local Similarity 29.2%; Pred. No. 2.8e-20;
Matches 78; Conservative 27; Mismatches 86; Indels 76; Gaps 11;

QY 10 VRKNEKSSGIN-----ASSASKERT-APLKSNT-GPPKLLCASLIFFLLAIS 60
DB 70 VTERDSENFSTNVAEIQALTSSGSSLEETIASLKAEEGFKORQAGV----- 119
QY 61 FFIAFVIFQYKYSOLLEKTKELVHTTECVKKNMPVE----- 99
DB 120 -----SEQETTTOKAHLGHCPCPVCPVHSMMLLRVQQLVQDLKLTCTQV 167
QY 100 -----ETAWSCCPKMKSFSSNCYFISTESASMODESKDCARMAHLVINTQEOE 152

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Db      168  ATINNASTEGTCCPYNNWEHODSCYWFSGSGMSMAEAERYCOLKNAHLVINSREQNF 227
QY      153  IFONLOESAY-FVGLSDPEGORHQMVDOTPYNESSTFWHHPREPSD-----PNERCV 204
Db      228  VOKYL--GSATYTMGLSDPEGA--WKWVDGTDYATGFQNNKPGQPDPMOCHGLGGEDCA 283
QY      205  VLNFRKSPKRMGNNDVNCJGPORSVCE 231
Db      284  --HFHPDGR--WDDVDCORPYHWCE 305
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Search completed: August 4, 2003, 13:12:15
Job time : 31 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 4, 2003, 13:10:58 ; Search time 52 Seconds

(without alignments)
541.270 Million cell updates/sec

Title: US-09-862-802-2

Perfect score: 1280
Sequence: 1 MTSSEITFAEVRKNEFKSSG.....NDVNCIGPQSRVCEMKIKH 237

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubppa/PCIT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/2/pubppa/PCITUS_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep:*
- 7: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
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- 17: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1280	100.0	237	10	US-09-862-802-2
2	1273	99.5	237	10	US-09-870-759-49
3	1267	99.0	243	9	US-09-764-870-464
4	1267	99.0	243	15	US-10-125-540-464
5	1267	99.0	246	9	US-09-764-870-303
6	1267	99.0	246	15	US-10-125-540-303
7	612.5	52.5	238	10	US-09-862-802-8
8	552	43.1	211	15	US-10-220-946-22
9	551.5	43.1	213	14	US-10-090-466-2
10	534.5	41.8	182	14	US-10-220-946-20
11	330	25.8	219	10	US-09-909-320-377
12	330	25.8	219	10	US-09-909-0888-377
13	330	25.8	219	10	US-09-905-291A-377
14	330	25.8	219	10	US-09-965-529-3
15	330	25.8	219	10	US-09-965-529-3

16	330	25.8	219	10	US-09-902-853-377	Sequence 377, App
17	330	25.8	219	10	US-09-907-824-377	Sequence 377, App
18	330	25.8	219	10	US-09-907-841-377	Sequence 377, App
19	330	25.8	219	11	US-09-904-011-377	Sequence 377, App
20	330	25.8	219	11	US-09-906-742-377	Sequence 377, App
21	330	25.8	219	11	US-09-906-838-377	Sequence 377, App
22	330	25.8	219	11	US-09-907-613-377	Sequence 377, App
23	330	25.8	219	11	US-09-907-942-377	Sequence 377, App
24	330	25.8	219	11	US-09-904-859-377	Sequence 377, App
25	330	25.8	219	11	US-09-909-204-377	Sequence 377, App
26	330	25.8	219	11	US-09-904-820-377	Sequence 377, App
27	330	25.8	219	11	US-09-904-746-377	Sequence 377, App
28	330	25.8	219	11	US-09-906-646-377	Sequence 377, App
29	330	25.8	219	11	US-09-906-700-377	Sequence 377, App
30	330	25.8	219	11	US-09-903-786-377	Sequence 377, App
31	330	25.8	219	11	US-09-902-903-377	Sequence 377, App
32	330	25.8	219	11	US-09-903-749A-377	Sequence 377, App
33	330	25.8	219	11	US-09-904-119-377	Sequence 377, App
34	330	25.8	219	11	US-09-904-956-377	Sequence 377, App
35	330	25.8	219	11	US-09-902-736-377	Sequence 377, App
36	330	25.8	219	11	US-09-907-794-377	Sequence 377, App
37	330	25.8	219	11	US-09-903-943-377	Sequence 377, App
38	330	25.8	219	11	US-09-904-462-377	Sequence 377, App
39	330	25.8	219	11	US-09-907-925-377	Sequence 377, App
40	330	25.8	219	11	US-09-902-692-377	Sequence 377, App
41	330	25.8	219	11	US-09-903-520-377	Sequence 377, App
42	330	25.8	219	11	US-09-905-056-377	Sequence 377, App
43	330	25.8	219	11	US-09-909-064-377	Sequence 377, App
44	330	25.8	219	11	US-09-904-553-377	Sequence 377, App
45	330	25.8	219	11	US-09-905-381-377	Sequence 377, App

ALIGNMENTS

RESULT 1
US-09-862-802-2
Sequence 2, Application US/09862802
Patent No. US20020165346A1
GENERAL INFORMATION:
APPLICANT: Schering-Plough Corporation
TITLE OF INVENTION: MAMMALIAN MEMBRANE PROTEIN GENES; RELATED REAGENTS
FILE REFERENCE: SF0695B
CURRENT APPLICATION NUMBER: US/09/862,802
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/111,470
PRIOR FILING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 237
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: mammalian protein
US-09-862-802-2

Query Match 100.0%; Score 1280; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 9, 7e-122;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTSSEITFAEVRKNEFKSSGINTASSAASERTAPLKSNTGFPKLCASLIIFLLAIS	60
DB	1	MTSSEITFAEVRKNEFKSSGINTASSAASERTAPLKSNTGFPKLCASLIIFLLAIS	60
QY	61	FFIAFVFFPKYSQLEKTKTKELVHTTLCVKNMPEETANSCCPKNNKSFSSNCFYI	120
DB	61	FFIAFVFFPKYSQLEKTKTKELVHTTLCVKNMPEETANSCCPKNNKSFSSNCFYI	120
QY	121	STESASWDSKDCARAEHLIVNTOEDFITQNLQESATFVGLSDPEGCRHWQVD	180
DB	121	STESASWDSKDCARAEHLIVNTOEDFITQNLQESATFVGLSDPEGCRHWQVD	180

OY 181 QTPNESSTFWHPRESDPNERCVLVNFRKSPKRMGMDVNCGQPRSCSEMAKIHL 237
|||||
D6 181 QTPNESSTFWHPRESDPNERCVLVNFRKSPKRMGMDVNCGPQRSCSEMAKIHL 237

RESULT 2
ME-00-97

```

US-09-870-759-49
Sequence 49, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
EO ID NO 49
LENGTH: 237
Type: PRt
ORGANISM: Homo sapiens
US-09-870-759-49

```

Query Match	99.5%	Score 1273;	DB 10,	Length 237;
Best Local Similarity	99.6%	Pred. No. 5e-121;		
Matches 236; Conservative	0;	Mismatches	1;	Indels 0; Gaps 0

QY	1	MTSELTAYEAVFPRKNEFKSSGINTASSAASKRETAPLKSNTPGPKLKASILIEFLLAIS	60
Db	1	MTSELTAYEAVFPRKNEFKSSGINTASSAASKRETAAPHKSNTPGPKLKASILIEFLLAIS	60
QY	61	FFIAFVIFEFQYSSQLLEKRTTRELVTHTLLECYKKNMPEYETAMSCCPKNNKSFSSNCYFI	120
Db	61	FFIAFVIFEFQYSSQLLEKRTTRELVTHTLLECYKKNMPEYETAMSCCPKNNKSFSSNCYFI	120
QY	121	STESASWODSEKDCARMEAHLLVINTQEBODIFIONLOESAYFWGLSDPESQRMOWMD	180
Db	121	STESASWODSEKDCARMEAHLLVINTQEBODIFIONLOESAYFWGLSDPESQRMOWMD	180
QY	181	QTPVNESSTFWMPRPSPDNERCQVLANRKSFKRKGAMDVYNOLGQORSVCENMKTHL	237
Db	181	QTPVNESSTFWMPRPSPDNERCQVLANRKSFKRKGAMDVYNOLGQORSVCENMKTHL	237

RESULT 3

```

US-764-870-464
Sequence 464, Application US/09764870
: Patent No. US20020042386A1
: GENERAL INFORMATION:
:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: p714
: CURRENT APPLICATION NUMBER: US/09/764,870
: CURRENT FILING DATE: 2001-01-17
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 646
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 464
: LENGTH: 243
: TYPE: prt
: ORGANISM: Homo sapiens
US-09-764-870-464

```

Query Match	99.0%;	Score 1267;	DB 9;	Length 243;
Best Local Similarity	99.6%;	Pred. No. 2.1e-120;		
Matches 234;	Conservative	0;	Indels	0;
		1;	Mismatches	0

```

OY      3 SEITAEVREKNEFKSSGININTSSAASKERTAPLKSNTGPKLLCASLITFFLLAISFF 62
          :|||||
DB      9 AEITAEVRFKNEFKSSGININTSSAASKERTAPLKSNTGPKLLCASLITFFLLAISFF 68

```

Qy 63 IAFVIFQKYSQLEKKTKTELVTTLCEYAKNMPVEETAMSCCPKNMKSFESSNCYFIST 122
|||||
Db 69 IAFVIFQKYSQLEKKTKTELVTTLCEYAKNMPVEETAMSCCPKNMKSFESSNCYFIST 128

Qy	123	ESASMODSEKDCARMAHILVINTQEOEPIQONLOESAFVGLSPDEGRHMQWDT	182
Db	129	ESASMODSEKDCARMAHILVINTQEOEPIQONLOESAFVGLSPDEGRHMQWDT	188
Qy	183	PYNESSFTFWHPREPSPDNRCYVLANFRKSPKRWGNVNCJGPOBSVCEMMKITH	237
Db	189	PYNESSFTFWHPREPSPDNRCYVLANFRKSPKRWGNVNCJGPOBSVCEMMKITH	243

QY 183 PYNESSTWHPREPSDPNERCVLNFNRKSPKRGMGNDVNCIGPQSSVCEMMKIH 237
|||||
Db 189 PYNESSTWHPREPSDPNERCVLNFNRKSPKRGMGNDVNCIGPQSSVCEMMKIH 243

RESULT 4

```

US-10-125-540-464
Sequence 464, Application US/10125540
Publication No. US20030059875A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTA1401
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 464
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
US-10-125-540-464

```

Query Match	99.0%	Score 1267	DB 15	Length 243
Best Local Similarity	99.6%	Pred. No. 2.1e-120		
Matches 234	Conservative 1	Mismatches 0	Indels 0	Gaps 0

QY	3	SEITVAEVRKNEFKSSGINTASSAASKRTPAPLSNNGPRLCLASLLIFLLALTSIF	62
QY	9	AEITVAEVRKNEFKSSGINTASSAASKRTPAPLSNNGPRLCLASLLIFLLALTSIF	68
QY	63	IAFVIFFOKYSOLLEKTKTRELHVTTLDECVRKNMPEVEATNSCCPKNMKSSESSNCYEIST	122
Db	69	IAFVIFFOKYSOLLEKTKTRELHVTTLDECVRKNMPEVEATNSCCPKNMKSSESSNCYEIST	128
QY	123	ESASWDSDEDCARMAHLIVINTQEODFITQNLQESATFVGLSPDEGRHMQWDT	182
Db	129	ESASWDSDEDCARMAHLIVINTQEODFITQNLQESATFVGLSPDEGRHMQWDT	188
QY	183	PYNSSSTFWHPRSPDNRCVYLNFRKSPKRMGNDVNCJGPOHSVCEMMKITH	237
Db	189	PYNSSSTFWHPRSPDNRCVYLNFRKSPKRMGNDVNCJGPOHSVCEMMKITH	243

RESULT 5

```

US-09-/764-8/0-303
: Sequence 303, Application US/09764870
: Patent No. US20020042386A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PT114
: CURRENT APPLICATION NUMBER: US/09/764,870
: CURRENT FILING DATE: 2001-01-17
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 646
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 303
: LENGTH: 246
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-764-870-303

```

Query match 99.08; Score 1267; DB 9; Length 246;

Best Local Similarity 99.6%; Pred. No. 2,1e-120;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SETTYAEVRKNEFKSSGINTASSASKERTAPLKSNTGPKLLCASLIFLLAISFF 62
Db 12 AETTYAEVRKNEFKSSGINTASSASKERTAPLKSNTGPKLLCASLIFLLAISFF 71
QY 63 IAFVIFFOKYSQLEKKTRELVTLECYKKNMPVEETAMSCCPKMKSFSSNCFIST 122
Db 72 IAFVIFFOKYSQLEKKTRELVTLECYKKNMPVEETAMSCCPKMKSFSSNCFIST 131
QY 123 ESASWQDSEKDCARMEAHLLVINTQEOEDIFONLOESAYFVGLSDPEGQRHMOVDOT 182
Db 132 ESASWQDSEKDCARMEAHLLVINTQEOEDIFONLOESAYFVGLSDPEGQRHMOVDOT 191
QY 183 PYNESSTFWHPRPSDPNERCVLNFRRKSPKRGMDVNCGLGQRSVCCEMKIHL 237
Db 192 PYNESSTFWHPRPSDPNERCVLNFRRKSPKRGMDVNCGLGQRSVCCEMKIHL 246

RESULT 6

Sequence 303, Application US/10125540
Publication No. US20030059875A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, proteins, and Antibodies
FILE REFERENCE: PTZ14C1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 303
LENGTH: 246
TYPE: PRT
ORGANISM: Homo sapiens
US-10-125-540-303

Query Match 99.0%; Score 1267; DB 15; Length 246;
Best Local Similarity 99.6%; Pred. No. 2.1e-120;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SETTYAEVRKNEFKSSGINTASSASKERTAPLKSNTGPKLLCASLIFLLAISFF 62
Db 12 AETTYAEVRKNEFKSSGINTASSASKERTAPLKSNTGPKLLCASLIFLLAISFF 71
QY 63 IAFVIFFOKYSQLEKKTRELVTLECYKKNMPVEETAMSCCPKMKSFSSNCFIST 122
Db 72 IAFVIFFOKYSQLEKKTRELVTLECYKKNMPVEETAMSCCPKMKSFSSNCFIST 131
QY 123 ESASWQDSEKDCARMEAHLLVINTQEOEDIFONLOESAYFVGLSDPEGQRHMOVDOT 182
Db 132 ESASWQDSEKDCARMEAHLLVINTQEOEDIFONLOESAYFVGLSDPEGQRHMOVDOT 191
QY 183 PYNESSTFWHPRPSDPNERCVLNFRRKSPKRGMDVNCGLGQRSVCCEMKIHL 237
Db 192 PYNESSTFWHPRPSDPNERCVLNFRRKSPKRGMDVNCGLGQRSVCCEMKIHL 246

RESULT 7

US-09-862-802-8
Sequence 8, Application US/09862802
Patent No. US20020165346A1
GENERAL INFORMATION:
APPLICANT: Schering-Plough Corporation
TITLE OF INVENTION: MAMMALIAN MEMBRANE PROTEIN GENES; RELATED REAGENTS
FILE REFERENCE: SF0695B
CURRENT APPLICATION NUMBER: US/09/862,802
CURRENT FILING DATE: 2002-01-10
Prior Application Number: US 09/111,470
Prior Filing Date: 1998-07-08
NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patent In version 3.1
SEQ ID NO 8
LENGTH: 238
TYPE: PRT
ORGANISM: unknown
FEATURE:
OTHER INFORMATION: mammalian protein
US-09-862-802-8

Query Match 52.5%; Score 672.5; DB 10; Length 238;
Best Local Similarity 53.3%; Pred. No. 3.7e-60;
Matches 129; Conservative 37; Mismatches 67; Indels 9; Gaps 6;

QY 1 MTEITYAEVRKNEFKSSGINTASSASKERTAPLKS--NTGPKLLCASLIFLLAISFF 58
Db 1 MASEITYAEVRKNE--SNSLHTYSESPAPRKRPIRLDKRPPSPILLSTLMLLLILA 58
QY 59 ISEFFIAVFIFFOKYSQLE--EKKTTRELVTLECYKKNMPVEETAMSCCPKMKSFSSNCFIST 117
Db 59 ITFLVAFIIFYOKYSQLEEKRAKKNIMHNLNCTKSVSPMEDKVMSCCPKMDRLFGSHC 118
QY 118 YFIST--ESASWQDSEKDCARMEAHLLVINTQEOEDIFONLOESAYFVGLSDPEGQRH 175
Db 119 YLVPVSSSSASMKSEKNCRMGAHLVIOEOEDIFITGLTTHAAYFGLWD--TGRHQ 177
QY 176 WQWVDOTPYNESSTFWHPRPSDPNERCVLNFRRKSPKRGMDVNCGLGQRSVCCEMKI 235
Db 178 WQWVDOTPYNESSTFWHNGEPSSNGEKATIIIRWK--TGGMWDISCLKQKVCQMKKI 236
QY 236 HL 237
Db 237 NL 238

RESULT 8

US-10-220-946-22
Sequence 22, Application US/10220946
Publication No. US20030124575A1
GENERAL INFORMATION:
APPLICANT: NO. US20030124575A1artlis AG
APPLICANT: No. US20030124575A1artlis Erfindungen Verwaltungsgesellschaft m.b.H.
APPLICANT: Phares, William
APPLICANT: Werner, Gudrun
APPLICANT: Jartz, Markus
APPLICANT: Lapp, Hilmar
APPLICANT: Kalthoff, Frank Stephan
TITLE OF INVENTION: Organic Compounds
FILE REFERENCE: 4-31347 PCT
CURRENT APPLICATION NUMBER: US/10/220,946
CURRENT FILING DATE: 2002-09-06
Prior Application Number: US 60/192,934
Prior Filing Date: 2000-03-29
Prior Application Number: US 60/205,026 (US 60/279,243)
Prior Filing Date: 2000-05-18
Prior Application Number: US 60/205,020
Prior Filing Date: 2000-05-18
Prior Application Number: US 60/205,769
Prior Filing Date: 2000-05-19
Prior Application Number: US 60/205,767
Prior Filing Date: 2000-05-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 211
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-220-946-22

Query Match 43.1%; Score 552; DB 15; Length 211;
Best Local Similarity 47.7%; Pred. No. 5.2e-48;
Matches 102; Conservative 42; Mismatches 60; Indels 10; Gaps 4;

QY 28 ASKERTAPLKSNTGPKLLCASLIFLLAISFFIAFVI---FQKYSQLEKKTKE 83

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Db 4 ASEDDE---KGLMWOLKYMAMVAVSILLSCFVSSVPHNFMYSKVKLSKIREQ 60
QY 84 LVHTLECVKKNMPEETAMSCCPKMKSSNCYFISTESAMODSEKCARMEAHILY 143
Db 61 QYHPLTCVMEKDIED--WSCCPYMTSFOSSCYFISTGMSQKNCSCVMGADLV 118
QY 144 INTOEODIFONLOESAYFVGLSDPEGQRHMWVDOTPYNESSTFMHPRSPDNERC 203
Db 119 INTREODFIIONLRNNSYFLGLSDPGRHMWVDOTPYNEVENTFMHSGEPNLDERC 178
QY 204 VVLRNRSKPKRMGMDVNCGLGFORSCVCEMKIHL 237
Db 179 ALINFRSS-EEMGWMDIHCHVPOKSIKMKKIYI 211

RESULT 9
US-10-090-466-2
Sequence 2, Application US/10090466
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
APPLICANT: Cullinan, Emily B.
TITLE OF INVENTION: NO. US20020137914A1 Human Declin Proteins and Polynucleotides
FILE REFERENCE: LEX-0315-USA
CURRENT APPLICATION NUMBER: US/10/090,466
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/274,961
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 213
TYPE: PRN
ORGANISM: homo sapiens
US-10-090-466-2

Query Match 43.1%; Score 551.5; DB 14; Length 213;
Best Local Similarity 50.8%; Pred. No. 6e-48;
Matches 97; Conservative 38; Mismatches 49; Indels 7; Gaps 3;

QY 51 LIFLLAISFIATV----FQKYSQLEKTKTELVTLECYKKNMPEETAMSCC 106
Db 26 VVSIILLSCFVSSVPHNFMYSKVKLSKIREQYQYHPLTCVMEKDIED--WSCC 83
QY 107 PKNMKSFCSSNCYFISTESAMODSEKCARMEAHILVINTREODFIIONLOESAYFVG 166
Db 84 PTPMWSFOSSCYFISTGMSQKNCSCVMGADLVINTREODFIIONLRNNSYFLG 143
QY 167 LSDPGRHMWVDOTPYNESSTFMHPRSPDNERCVVLRNRSKPKRMGMDVNCGLGPO 226
Db 144 LSDPGRHMWVDOTPYNEVENTFMHSGEPNLDERCALINFRSS-EEMGWMDIHCHVPO 202
QY 227 RSVCEMKIHL 237
Db 203 KSIKMKKIYI 213

RESULT 10
US-10-220-946-20
Sequence 20, Application US/10220946
GENERAL INFORMATION:
APPLICANT: No. US20030124575A1artlis AG
APPLICANT: No. US20030124575A1artlis Erfindungen Verwaltungsgesellschaft m.b.H.
APPLICANT: Phares, William
APPLICANT: Werner, Gudrun
APPLICANT: Jaritz, Markus
APPLICANT: Lapp, Hilmar
APPLICANT: Kalchoff, Frank Stephan
TITLE OF INVENTION: Organic Compounds
FILE REFERENCE: 4-31347 PCT
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QY 107 PKNMKSFCSSNCYFISTESAMODSEKCARMEAHILVINTREODFIIONLOESAYFVG 166
Db 84 PTPMWSFOSSCYFISTGMSQKNCSCVMGADLVINTREODFIIONLRNNSYFLG 143
QY 167 LSDPGRHMWVDOTPYNESSTFMHPRSPDNERCVVLRNRSKPKRMGMDVNCGLGPO 226
Db 144 LSDPGRHMWVDOTPYNEVENTFMHSGEPNLDERCALINFRSS-EEMGWMDIHCHVPO 202
QY 227 RSVCEMKIHL 237
Db 203 KSIKMKKIYI 218

RESULT 11
US-10-090-466-4
Sequence 4, Application US/10090466
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
APPLICANT: Cullinan, Emily B.
TITLE OF INVENTION: NO. US20020137914A1 Human Declin Proteins and Polynucleotide
FILE REFERENCE: LEX-0315-USA
CURRENT APPLICATION NUMBER: US/10/090,466
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/274,961
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 182
TYPE: PRN
ORGANISM: homo sapiens
NAME/KEY: VARIANT
LOCATION: (1)...(182)
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-090-466-4

Query Match 41.8%; Score 534.5; DB 14; Length 182;
Best Local Similarity 54.4%; Pred. No. 2.6e-46;
Matches 92; Conservative 31; Mismatches 43; Indels 3; Gaps 2;

QY 69 FQKYSQLEKTKTELVTLECYKKNMPEETAMSCCPKMKSSNCYFISTESAMQ 128
```

Db 17 YSKTVRLSKLREYQYHXLTCVMECKDIED--WSCCPYMTWTFQSSCYFISTGMQSWT 74
QY 129 DSEKCARMEAHLLVINTQEDPFITONLOESAYFVGLSDPESQRHMVNDOPVYESS 188
Db 75 KSKQNSVKGADLVYITREODITIONLRNSSYFLGLSDPGGRHMVNDOTPYNEVY 134
QY 189 TFWHPRPSDPNRCVVLNFRKSPKRWGMNDVNCGLQFQSRVCEMMKITHL 237
Db 135 TFWHSGEPNNLDERCALINFRSS-EEWGMNDHCHVQKSKCKKKTIVY 182

RESULT 12
US-09-909-320-377
Sequence 377, Application US/09909320
Patent No. US20020132240A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,320
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 377
LENGTH: 219
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-320-377

Query Match 25.8%; Score 330; DB 10; Length 219;
Best Local Similarity 38.0%; Pred. No. 1.8e-25;
Matches 70; Conservative 29; Mismatches 79; Indels 6; Gaps 3;

QY 55 LLTAISFFIAVFIFQKYSOLEKRTKELVHTLECVKRNMPVEETAWSCCPKRNKFS 114
Db 32 LFLSACFTTRCYVTFRIFQCODEKKFOLPENFTFLSCYNG---SGSVKNCCPLNMWYFQ 88
QY 115 SNCYFISTESASWODEKDCARMEAHLLVINTQEDPFITONLOESAYFVGLSDPEGQR 174
Db 89 SSCYFFSTDTISWALSILKNCSSAMGAHLVINSQEOEFLSYKKPKMREFFIGLSDQYVEG 148
QY 175 HMCVNDOTPYNESTFWHPRPSD--PNERCVVLNFRKSPKRWGMNDVNCGLQFQSRVCEM 232
Db 149 QMCVNDOTPLTKSLSFWDVGPNNIATLEDCATIRDSNP-RQNMNDVTCGLNFRICEM 207
QY 233 MKIH 236
Db 208 VGIN 211

RESULT 13
US-09-909-088B-377
Sequence 377, Application US/09909088B
Patent No. US20020146709A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048


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QY 175 HHOVDOQPTYNESSTFHHREPSD--PNBRCVVLNFRKSPKRWGNIYVNCJGPQRCVGM 232
    ||||| : : : ||| : : : ||| : : : ||| : : : |||
Db 149 QMOWDGFPLTNSLSSTWMDVGEPPNNTATLEDCATMDSSNP-RQNNVDYTCFLNFRICEM 207
    ||| : : : ||| : : : ||| : : : ||| : : : |||
QY 233 MKIH 236
    : : : ||| : : : ||| : : : ||| : : : |||
Db 208 VGIN 211

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RESULT 15

```

US-09-965-529-3
; Sequence 3, Application US/09965529
; Publication No. US20020182671A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LO, Dyung Alina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PP-0731 USA
; CURRENT APPLICATION NUMBER: US/09/965,529
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ. ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 1521513CD1
US-09-965-529-3

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Query Match	25.8%;	Score 330;	DB 10;	length 219;
Best Local Similarity	38.0%;	Pred. No. 1.8e-25;		
Matches 70; Conservative	29;	Mismatches 79;	Indels 6;	Gaps 3

[illegible]

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Search completed: August 4, 2003, 13:20:02
Job time : 54 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 13:05:58 ; Search time 40 Seconds
(without alignments)
569,799 Million cell updates/sec

Title: US-09-862-802-2

Perfect score: 1280

Sequence: 1 MTSEITYAEVRFKNEKSSG.....NDVNCIGPQSVCEMMKIHLL 237

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1280	100.0	237	2 JC7608	type II lectin-like
2	251	19.6	301	2 SI3165	asialoglycoprotein
3	235	18.4	301	1 LNRT2	hepatic lectin 2 -
4	228.5	17.9	284	1 LNRTL	hepatic lectin - r
5	227.5	17.8	306	2 A42230	lectin M-ASGP-BP P
6	224	17.5	207	1 LNCHL	hepatic lectin - c
7	223.5	17.5	311	1 LNHD2A	asialoglycoprotein
8	221	17.3	284	2 S29855	asialoglycoprotein
9	220.5	17.2	291	1 LNHD1	hepatic lectin HI
10	219.5	17.1	742	2 JC7595	scavenger receptor
11	216.5	16.9	304	2 JX0209	lectin, galactose/
12	208.5	16.3	331	1 LNMSER	IgE Fc receptor, 1
13	207	16.2	1479	2 T42710	IgE Fc receptor, 1
14	205.5	16.1	309	1 S34198	mannose receptor, II
15	205.5	16.1	404	2 A46274	HIV gp120-binding
16	196	15.3	350	2 A28166	neupifer cell recep
17	187	14.6	1268	2 S52781	neurocan - mouse
18	184	14.4	1257	2 S28764	neurocan precursor
19	183.5	14.3	2124	2 A28452	proteoglycan core
20	181	14.1	1340	2 A39808	proteoglycan core
21	181	14.1	2327	2 T42630	aggreacan - bovine
22	176	13.8	2109	1 T50421	aggreacan precursor
23	176	13.8	2132	1 A55182	aggreacan precursor
24	176	13.8	2415	1 A39086	NKR-p1 protein hom
25	175.5	13.7	220	2 C46467	reg II, regenerati
26	174	13.6	173	2 B47148	mannose receptor p
27	172.5	13.5	1455	1 A48925	mannose receptor p
28	171.5	13.4	1456	1 A36563	mannose receptor p
29	171	13.4	266	2 I49059	Ly49c - mouse

30	170.5	13.3	155	2 S78774	perilucan - Haloti
31	170	13.3	223	2 B46467	NKR-p1 protein hom
32	169	13.2	257	2 I50146	gene 17.5 protein
33	168	13.1	883	2 S57653	brevican precursor
34	168	13.1	3562	2 A47171	chondroitin sulfate
35	167	13.0	153	1 A34313	antifreeze protein
36	167	13.0	173	2 S10548	lectin - baracle
37	167	13.0	216	2 PT0375	natural killer cel
38	167	13.0	912	2 A54423	brevican precursor
39	166	13.0	330	2 T46256	brevican human (
40	165.5	12.9	321	1 LNHDUR	IgE Fc receptor II
41	165	12.9	883	2 S49126	brevican precursor
42	164	12.8	223	2 A35917	NK-cell receptor p
43	162.5	12.7	227	2 A46467	natural killer cel
44	159.5	12.5	162	1 LNRC3	lectin-BRA3-2 prec
45	157	12.3	266	2 I49363	natural killer cel

ALIGNMENTS

```

RESULT 1
JC7608
Type II lectin-like immunoreceptor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7608
R: Huang, X.; Yuan, Z.; Chen, G.; Zhang, M.; Zhang, W.; Yu, Y.; Cao, X.
Biochem. Biophys. Res. Commun. 281, 131-140, 2001
A:Title: Cloning and characterization of a novel ITIM containing lectin-like immunore
A:Reference number: JC7608; MUID:21092797; PMID:11178971
A:Contents: Dendritic cells
A:Accession: JC7608
A:Molecule type: mRNA
A:Residues: 1237 <HDA>
A:Cross-references: GB:AF067800
C:Comment: This receptor, highly homologous to the group of macrophage/hepatic lectin
cell, especially in migrating, antigen capturing and processing.
C:Genetics:
A:Gene: 111r
A:Map position: 12p13
F:45-69/Domain: transmembrane #status predicted <TMM>

Query Match      100.0% Score 1280; DB 2; Length 237;
Best Local Similarity 100.0%; Pred No. 1.4e-105;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTSEITYAEVRFKNEKSSGINTASSAASKERTAPLKSNTGPKLLCASLIFLLAIS 60
      |||||||
Db      1 MTSEITYAEVRFKNEKSSGINTASSAASKERTAPLKSNTGPKLLCASLIFLLAIS 60
      |||||||

QY      61 FFIAFYFFQKYSQLEKTKTKELVHTTLECVKKNMPVEETANSCCPKMKSSSCYFI 120
      |||||||
Db      61 FFIAFYFFQKYSQLEKTKTKELVHTTLECVKKNMPVEETANSCCPKMKSSSCYFI 120
      |||||||

QY      121 STFSASMODESKCARNEAHLVINTQEBDFTFQNLQESATFVGLSPDEGRHQMWD 180
      |||||||
Db      121 STFSASMODESKCARNEAHLVINTQEBDFTFQNLQESATFVGLSPDEGRHQMWD 180
      |||||||

QY      181 QTPYNNSSTFWHDREPSDPERNCVNLNFRKSPRKMGMNDVNCIGPQSVCEMMKIHLL 237
      |||||||
Db      181 QTPYNNSSTFWHDREPSDPERNCVNLNFRKSPRKMGMNDVNCIGPQSVCEMMKIHLL 237
      |||||||

RESULT 2
SI3165
asialoglycoprotein receptor - mouse
N:Alternate names: hepatic lectin
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C:Accession: SI3165
R:Sanford, J.P.; Doyle, D.
Biochim. Biophys. Acta 1087, 259-261, 1990

```

A>Title: Mouse asialoglycoprotein receptor cDNA sequence: conservation of receptor genes
 A:Reference number: S13165; MUID:91027942; PMID:2223888
 A:Accession: S13165
 A:Molecule type: mRNA
 A:Residues: 1-301 <SAS>
 A:Cross-references: EMBL:X53042; NID:953104; PIDN:CAA37211.1; PID:953105
 C:Superfamily: hepatic lectin; C-type lectin homology
 C:Keywords: glycoprotein; liver; transmembrane protein
 F:170-293/Domain: C-type lectin homology <LCH>

Query Match 19.6%; Score 251; DB 2; Length 301;
 Best Local Similarity 25.2%; Pred. No. 1.2e-14;
 Matches 65; Conservative 38; Mismatches 75; Indels 80; Gaps 7;

42 FPKLLASLLIFLLAISFFIAFYI-----FFQKYS----- 73
 49 FPKRLCSFRLSLALANILLVIVCVSSOSIOLOEERFLKETFNSFSSSTLMERGA 108
 74 -----OLLEKKTKEIVHTTECVKKNMPV-----ETAMS 104
 109 LDTLGSTNAILTSMWADLEEKQOLKADHSTLFLHHPMDLRTILCOLAYFQSGTE 168
 105 CCPKMKSFSSNCYFISTESASWDSKDCARMEAHLLVINTOEODFIQNLQESAYF 164
 169 CCPVNWVEFGSGCYWFSDGLTMAADQYCOLENAHLVINSREODPVVKK-RSOFHIW 227
 165 VGLSDPEGQRHMQWQDTPYNESSTFWMPHREPSDNERCVVLPFKSPKRMG----- 216
 228 IGLTDRDGS--WKWVDGTEYRSNFRNMAFTQPD-----NMGGHGGGSEDCAEILIS 276
 217 ---WADVNCLEGPORSVCE 231
 277 DGHWNDFNCCQVNRWVACE 294

RESULT 3

LNRT2
 hepatic lectin 2 - rat

N:Alternate names: asialoglycoprotein receptor RHL-2/3 (ASGP-R2/3)

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Mar-1988 #sequence-revision 09-Apr-1998 #text-change 22-Jun-1999

C:Accession: B28462; A28462; A31601; A26888; A25417
 R:Halberg, D.F.; Wager, R.E.; Farrell, D.C.; Hildreth IV, J.; Quesenberry, M.S.; Loeb, J.

J. Biol. Chem. 262: 9628-9836, 1987
 A>Title: Major and minor forms of the rat liver asialoglycoprotein receptor are independent

A:Reference number: A28462; MUID:87250565; PMID:3597443
 A:Accession: B28462

A:Molecule type: mRNA
 A:Residues: 1-301 <HAL>

A:Cross-references: GB:J02762; NID:9205162; PIDN:AAA1522.1; PID:9205163
 A:Accession: A28462

A:Molecule type: protein
 A:Residues: 88-96, 'X', 98-118, 'X', 120-129-158-177-182, 'X', 184, 'X', 186-189, 192-290, 'C', 292

R:Sanford, J.P.; Elliott, R.W.; Doyle, D.
 DNA 7, 721-728, 1988

A>Title: Asialoglycoprotein receptor genes are linked on chromosome 11 in the mouse.
 A:Reference number: A31601; MUID:89170119; PMID:3234178

A:Accession: A31601
 A:Molecule type: mRNA

A:Residues: 1-301 <SAS>

A:Cross-references: GB:X07636; NID:957066; PIDN:CAA30476.1; PID:957067
 R:McPhaul, M.; Berg, P.

Mol. Cell. Biol. 7, 1841-1847, 1987
 A>Title: Identification and characterization of cDNA clones encoding two homologous prot

A:Reference number: A26888; MUID:87257885; PMID:3600647
 A:Accession: A26888

A:Molecule type: mRNA
 A:Residues: 1-152, 'A', 154-201, 'T', 203-259, 'C', 261-301 <MCP>

A:Cross-references: GB:M16347; NID:9206648; PIDN:AAA42038.1; PID:9206649
 A>Note: the authors translated the codon GCA for residue 153 as Arg and ATT for residue

R:Drickamer, K.; Memon, J.F.; Blinn, G.; Leung, J.O.
 J. Biol. Chem. 259, 770-778, 1984
 A>Title: Primary structure of the rat liver asialoglycoprotein receptor: structural evid

A:Reference number: A25417; MUID:84111554; PMID:6319386
 A:Accession: A25417
 A:Molecule type: protein
 A:Residues: 201-259, 'C', 261-281, 'ND', 284-301 <DRI>
 C:Comment: Calcium is required for ligand binding.
 C:Superfamily: hepatic lectin; C-type lectin homology
 C:Keywords: endocytosis; glycoprotein; lectin; liver; receptor; transmembrane protein
 F:2-60/Domain: intracellular #status predicted <INT>
 F:61-77/Domain: transmembrane #status predicted <TRN>
 F:78-301/Domain: extracellular #status predicted <EXT>
 F:170-293/Domain: C-type lectin homology <LCH>
 F:97,119,165/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 18.4%; Score 235; DB 1; Length 301;
 Best Local Similarity 25.6%; Pred. No. 3.1e-13;
 Matches 66; Conservative 39; Mismatches 73; Indels 80; Gaps 11;

42 FPKLLASLLIFLLAISFFIAFYI-----FKR----- 71
 49 FPKRLCSFRLSLALANILLVIVCVSSOSMOLOEFTLKEFLSNFSTTLMEFKA 108
 72 -----YSOLLEKKTKEIV--HTTECVKKNMPVE-----ETAM 103
 109 LDSHGSRNNDITSWETLEKK-QDKIKADHSTLFLHKKHPDLRTILCOLAFPLSNGT 167
 104 SCCPKMKSFSSNCYFISTESASWDSKDCARMEAHLLVINTOEODFIQNLQESAY 163
 168 ECCPVNWVEFGSGCYWFSDGLTMAADQYCOMENAHLLVINSREGEFV---YKHGAF 224
 164 --FVGLSDPEGQRHMQWQDTPYNESSTFWMPHREPSD-----PNEGCV-VLNRKSPK 213
 225 HIWIGLTDKDS--WKWVDGTEYRSNFRNMAFTQPDNMGGHGGSEDCAEILISGL- 279
 214 RMGWNDFNCCQVNRWVACE 231
 280 ---WADVNCLEGPORSVCE 294

RESULT 4

LNRT1
 hepatic lectin - rat

N:Alternate names: ASGP; asialoglycoprotein receptor

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Feb-1986 #sequence-revision 04-Dec-1986 #text-change 22-Jun-1999

C:Accession: A92497; A94020; B94020; A54727; A03166
 R:Leung, J.O.; Holland, E.C.; Drickamer, K.

J. Biol. Chem. 260, 12523-12527, 1985
 A>Title: Characterization of the gene encoding the major rat liver asialoglycoprotein

A:Reference number: A92497; MUID:86008335; PMID:2995379
 A:Accession: A92497

A:Molecule type: DNA
 A:Residues: 1-284 <LEB>

A:Cross-references: GB:K02817; NID:9206646; PIDN:AAA42037.1; PID:9206647
 R:Holland, E.C.; Leung, J.O.; Drickamer, K.

Proc. Natl. Acad. Sci. U.S.A. 81, 7338-7342, 1984
 A>Title: Rat liver asialoglycoprotein receptor lacks a cleavable NH-2-terminal signal

A:Reference number: A94020; MUID:85063786; PMID:6095287
 A:Accession: A94020

A:Molecule type: mRNA
 A:Residues: 1-60, 'R', 62-210 <HOI>

A:Experimental source: clone 22; clone 1
 A:Accession: B94020

A:Molecule type: mRNA
 A:Residues: 92-284 <HO2>
 A>Note: clone 22 codes for a terminator at residue 210

R:Watts, C.
 Biosci. Rep. 6, 527-534, 1986

A>Title: Isolation and expression of cDNA clones for a rat liver asialoglycoprotein r
 A:Reference number: A54727; MUID:87026895; PMID:2945599

A:Accession: A54727
 A:Molecule type: mRNA

A:Residues: 12-284 <WAT>
 A:Cross-references: GB:M21770; NID:9202985; PIDN:AAA40764.1; PID:9202988

A:Experimental source: liver
C:Comment: Two types of rat hepatic lectin have been identified, RHL-1 and RHL-2/3, have
C:Comment: After removal of sialic acid monomers from the complex carbohydrate moieties
C:Comment: The unusual orientation of this protein across the membrane is postulated to
C:Genetics:
A:Introns: 23/1; 62/1; 118/1; 147/1; 197/3; 233/2
C:Species: hepatic lectin; C-type lectin homology
C:Superfamily: glycoprotein; lectin; receptor; transmembrane protein
F:2-284/Product: hepatic lectin #status predicted <MAY>
F:2-39/Domain: intracellular #status predicted <INT>
F:40-60/Domain: transmembrane #status predicted <EXT>
F:61-284/Domain: extracellular #status predicted <EXT>
F:153-276/Domain: C-type lectin homology <LCH>
F:75,78,146/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 17.9%; Score 228.5; DB 1; Length 284;
Best Local Similarity 23.6%; Pred. No. 1.1e-12;
Matches 61; Conservative 36; Mismatches 84; Indels 77; Gaps 8;

43 PKL---LCASLIFLLAIFFAFYF-----FQKYSQLEKTKTRELVT-----TLECVKKNMPYEE 100
28 PRLQRLCSGFRLLLSIGLSILLVYVCTTSQNSQLEDRVLRLQNFNFTVSTEDQV 87
69 -----FQKYSQLEKTKTRELVT-----TLECVKKNMPYEE 100
88 KALTQGERVGRKKMKLVESQLEKHQEDRLHVKQVSDVRSLSQMALRNG 147
QY 101 TAWSCCCKRNKSFSSNCFISTESASWQSDSEKDCARMEAHLLVINTQEDQFQNLQOE 160
148 SERICCPINWVEYSGCYWSSSVKVPTEADKCYOLENAHLLVYVTSWEGQRFVQOHMGPL 207
QY 161 SAVFVGLSDPEGQRHMQWVDQTPYNESSTFWHPREPSD-----PNERCVLNFRRKSPK 213
208 NTFM-IGLTDQNGP--WKWVDGTDYETGFKMRRPGQPDWYGHGLGGEDCA--HFTTDCG 262
QY 214 RWGNNDVNCGLGQPSVCE 231
263 ---WDDVYCRPRYRWCE 277

RESULT 5
A42230
A:Title: M-ASGP-BP precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 20-Aug-1999
C:Accession: A42230
R:11; M.; Kurata, H.; Itoh, N.; Yamashina, I.; Kawasaki, T.
J. Biol. Chem. 265, 11295-11298, 1990
A:Title: Molecular cloning and sequence analysis of cDNA encoding the macrophage lectin
A:Accession: A42230; MUID:90293078; PMID:2358462
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-306 <I>
A:Cross-references: GB:J05495; NID:9204302; PID:AAA41216.1; PID:9204303
C:Superfamily: hepatic lectin; C-type lectin homology
F:175-298/Domain: C-type lectin homology <LCH>

Query Match 17.8%; Score 227.5; DB 2; Length 306;
Best Local Similarity 31.6%; Pred. No. 1.4e-12;
Matches 48; Conservative 27; Mismatches 62; Indels 15; Gaps 5;

88 TLECVKKNMPYEEAWSCCPKRNKSFSSNCFISTESASWQSDSEKDCARMEAHLLVINTQ 147
Db 157 TLTQQLASLNKNGSAVACCPHMHMHESGCTWFSQSGKWPPEADKYCOLENSNLVYVNSL 216
QY 148 EEDQFIFQNLQOEASAFVGLSDPEGQRHMQWVDQTPYNESSTFWHPREPSD-----PN 200
Db 217 AEQMFLL-QTHGSVVVTWIGLTDQNGP--WRWVDGTDYETGFKMRRPGQPDWYGHGLGG 273
QY 201 ERCVYVLFRRKSPKRWGNNDVNCGLGQPSVCEM 232
Db 274 EDCA--HFTSDGR---WDDVYCRPRYRWCEM 300

RESULT 6
LNCHL
hepatic lectin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 08-Oct-1981 #sequence_revision 08-Oct-1981 #text_change 22-Jun-1999
C:Accession: A03167; A28194; A40427
R:Drickamer, K.
J. Biol. Chem. 256, 5827-5839, 1981
A:Title: Complete amino acid sequence of a membrane receptor for glycoproteins. Sequ
A:Reference number: A03167; MUID:81215504; PMID:7240175
A:Accession: A03167
A:Molecule type: protein
A:Residues: 1-207 <DR>
A>Note: some or all of the cysteines are involved in disulfide bonds
A>Note: residues 24-48 form an uncharged, hydrophobic region that may interact with o
J. Biol. Chem. 263, 5468-5473, 1988
A:Title: Endocytosis of N-acetylglucosamine-containing glycoproteins by rat fibroblas
A:Reference number: A28194; MUID:88186849; PMID:3281941
A:Accession: A28194
A:Molecule type: mRNA
A:Residues: 1-207 <ME>
A:Cross-references: GB:J03188; NID:9212246; PID:AAA48937.1; PID:9212247
R:Bezouska, K.; Crichton, G.V.; Rose, J.M.; Taylor, M.E.; Drickamer, K.
J. Biol. Chem. 266, 11604-11609, 1991
A:Title: Evolutionary conservation of intron position in a subfamily of genes encodin
A:Reference number: A40427; MUID:91268022; PMID:2050668
A:Accession: A40427
A:Molecule type: DNA
A:Residues: 1-207 <BE>
A:Cross-references: GB:M63225; GB:M63226; GB:M63227; GB:M63228; GB:M63229; GB:M63230;
C:Comment: Hepatic lectin is a membrane receptor protein that recognizes and binds ex
and endocytosis.
C:Genetics:
A:Introns: 15/1; 50/1; 75/1; 125/3; 163/2
C:Superfamily: hepatic lectin; C-type lectin homology
C:Keywords: acetylated amino end; glycoprotein; lectin; transmembrane protein
F:1-23/Domain: intracellular #status predicted <INT>
F:24-47/Domain: transmembrane #status predicted <TRA>
F:48-207/Domain: extracellular #status predicted <EXT>
F:78-201/Domain: C-type lectin homology <LCH>
F:1/Modified site: acetylated amino end (Met) #status experimental
F:67/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 17.5%; Score 224; DB 1; Length 207;
Best Local Similarity 27.8%; Pred. No. 1.9e-12;
Matches 54; Conservative 35; Mismatches 79; Indels 26; Gaps 7;

49 SLILFLLAIFFAFY---IFQKYSQLEKTKTRELVTTLTLECVKKNMPYEEAWSC 105
Db 24 SFAVYVLLALSFLLTLTLSSVSLARIALSSKLTLD-----SEPHNFSRSRLLEP 77
QY 106 C---PKRNKSFSSNCFISTESASWQSDSEKDCARMEAHLLVINTQEDQFQNLQOE 162
Db 78 CGAQRQMEYFEGKRYYSLSRMSWKKAKACEHSHLLIIDSVAKNFMYFRNRN-R 136
QY 163 YFVGLSDPEGQRHMQWVDQTPYNESSTFWHPREPSD--NERCVLNFRRKSPKRW--GW 217
Db 137 FWIGITDENQGEWQWVDGTDTRRSFTFWKEGEPNNGFNDCAHV-----WTSQW 188
QY 218 NDVNCGLGQPSVCE 231
Db 189 NDVYCTTECYVCE 202

RESULT 7
LNH2A
asialoglycoprotein receptor H2a - human
N:Alternate names: hepatic lectin H2a
N:Contains: ASGPR; asialoglycoprotein receptor H2a; asialoglycoprotein receptor H2b
C:Species: Homo sapiens (man)

A:Reference number: JX0209; MUID:92268032; PMID:1587794
A:Accession: JX0209
A:Molecule type: mRNA
A:Residues: 1-304 <SNAT>
A:CROSS-references: GB:S5676; NID:g249360; PIDN:AAB22171.1; PID:g249361
R:Oda, S.; Sato, M.; Toyoshima, S.; Osawa, T.
J. Biochem. 104, 600-605, 1988
A>Title: Purification and characterization of a lectin-like molecule specific for galactose
A:Reference number: PX0009; MUID:89197865; PMID:3241002
A:Accession: PX0009
A:Molecule type: protein
A:Residues: 102-120;137,'X',139-151 <ODA>
C:Superfamily: hepatic lectin; C-type lectin homology
F:36-61/Domain: transmembrane status predicted <TRA>
E:174,166/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 16.9%; Score 216.5; DB 2; Length 304;
Best Local Similarity 31.1%; Pred. No. 1.3e-11;
Matches 47; Conservative 25; Mismatches 64; Indels 15; Gaps 5;

Oy 89 LECKKKNPVETIAMSCPKRWKSFSSNCYITSTESASWQDSKDCAMEHLLVINTQE 148
.:
Db 156 LTCLDLANKNGSEVACCPHLMTHEGSCYWFSESSEKSWPADRYCCRLSHNLVVNSLE 215
.:
Oy 149 EODTIFONLQESAAYFVGLSPDEGORHMOWDOPNYNSSTFPMHPREPSD-----PNE 201
||| : || :
Db 216 EQNEL-QNRLANVSWIGLTQNGP -WRWDGDGFDFEGFNMAPILOPDNNFGHGLGGGE 272
.:
Oy 202 RCVALNFERSPEKRWGMNDVNCILGPORSVCEN 232
.:
Db 273 DCAHHT-TGGE----WNDDYCQRTEFRWICEM 298

RESULT 12
INMSER
I:IGE Fc receptor, low-affinity - mouse
N:Alternate names: Blast-2; CD23; Fc-epsilon-RII; lymphocyte IGE receptor
C:Species: Mus musculus (house mouse)
C>Date: 12-Feb-1993 #sequence_revision 28-Oct-1994 #text-change 22-Jun-1999
C:Accession: A43518; A33840
R:Golindick, S.O.; Tronustine, M.L.; Yamashita, L.C.; Kehry, M.R.; Moore, K.W.
J. Immunol. 144, 1974-1982, 1990
A>Title: Isolation, characterization, and expression of cDNA clones encoding the mouse
A:Reference number: A43518; MUID:90171598; PMID:2137845
A:Accession: A43518
A:Molecule type: mRNA
A:Residues: 1-331 <GOLO>
A:CROSS-references: GB:M4163; NID:g193242; PIDN:AA37603.1; PID:g309227
R:Bettler, B.; Hostetler, H.; Rao, M.; Yokoyama, W.M.; Kilcherr, F.; Conrad, D.H.
Proc. Natl. Acad. Sci. U.S.A. 86, 7566-7570, 1989
A>Title: Molecular structure and expression of the murine lymphocyte low-affinity recep
A:Reference number: A33840; MUID:90017519; PMID:2529542
A:Accession: A33840
A:Molecule type: mRNA
A:Residues: 1-331 <BEND>
A:CROSS-references: GB:M99371; NID:g193245; PIDN:AA74898.1; PID:g193246; GB:M27150
C:Comment: This receptor for the Fc portion of IGE is expressed in various hematopoietic
t B-cells.
C:Superfamily: IGE receptor II; C-type lectin homology
F:KeyWords: B-cell; glycoprotein; immunoglobulin receptor; macrophage; tandem repeat,
F:1-35/Domain: intracellular #status predicted <INT>
F:14-22/Region: stop-transfer sequence
F:26-46/Domain: transmembrane #status predicted <TM>
F:47-331/Domain: extracellular #status predicted <EXT>
F:66-86/Region: 21-residue repeat
F:87-107/Region: 21-residue repeat
F:108-128/Region: 21-residue repeat
F:129-149/Region: 21-residue repeat
F:186-305/Domain: C-type lectin homology <LCH>
F:65,114/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match Similarity 16.3%; Score 208.5; DB 1; Length 331;
Best Local Similarity 31.2%; Pred. No. 7.4e-11;
Matches 53; Conservative 34; Mismatches 60; Indels 23; Gaps 8;

75 LLEKTKELVHTTIECYVK---NMPVEETAMSCCPKMKSFSSNCYFISTESASWDS 130
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
151 INEKTATSDSLEKLOEEFAFKLMIELILISKGTACNICPKMWLHFOQKCXYFGKSGMOWIA 210
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
131 EKDCAFMRAHLIVINTGOEDFIIFONTLOEBSAYFVGSLDPGQRHMVNDOTPTNESSTF 190
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
211 RPACSEDLGRIVLSTHSOKEDPLMOCHINKKSW--IGLODLMMEGEFVSIDSIPVGYSN-- 267

OY 191 WHPREPSD--PNERCVVLNFRKSPKRMGMNVNCLGPORS-----VCCEAM 233
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 268 MNPGEPNNGGGEGDCVMN--RGSQG---WNDAFC----RSYLDMAVCEQL 308

RESULT 13
2710
mouse receptor, macrophage - mouse
Alternate names: lambda lectin; phospholipase A2 receptor
C.Species: Mus musculus (house mouse)
C.Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000
C.Accession: T42710
R.Wu, K.; Yuan, J.; Tasky, L.A.
J. Biol. Chem. 271, 21323-21330, 1996
A.Title: Characterization of a novel member of the macrophage mannose receptor type C lectin family: phospholipase A2 receptor; C-type lectin homology; fibronectin type II repeat domain; membrane protein; receptor
A.Reference number: Z22235; MUID:96355501; PMID:8702911
A.Accession: T42710
A>Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-1479 <MAX>
A.Cross-references: EMBL:U56734; NID:91336073; PID:91336074; PIDD:AAC52729.1
C.Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II repeat domain; membrane protein; receptor
F:186-227/Domains: fibronectin type II repeat homology <2Fr>

Query Match 16.2%; Score 207; DB 2; Length 1479;
Best Local Similarity 31.8%; Pred. No. 5.5e-10;
Matches 50; Conservative 27; Mismatches 54; Indels 26; Gaps 7;

91 CVKKN----MPEVEETAMSC---CPKNKMSFSNSCYFISTESASMODESKCARMEAHLL 142
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 358 CKKRKNATVEIDIQDRMTMVNAKECDPSMQPPQGHCRIRQAARKSRMGSKRCALGGDDL 417
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 143 VINTGOEDFIIFONTLOEBSAYFVGSLDPGQRHMVNDOTPTNESSTFWHPRPS---D 198
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
418 SIHSVAELEFTITKOKEVEBELTWGLNDLKQMNFWSDSGLV--SFTWHHPPEPNNRD 475

OY 199 PNERCVVLNFRKSPKRMG---NMVDNCLGPQRSCE 231
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 476 SLEDCTLT-----WGPEGRWMDSPCNOSLPISCK 504

RESULT 14
534198
Ige Fc receptor II, low-affinity - rat
N.Alternate names: CD23; lymphocyte Ige receptor
C.Species: Rattus norvegicus (Norway rat)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Jun-1999
C.Accession: S34198
R.Flores-Romo, L.; Sheld, J.; Humbert, Y.; Graber, P.; Aubry, J.P.; Gauchat, J.F.; Ayala, J.
Submitted to the EMBL Data Library, June 1993
A.Description: Inhibition of an in vivo antigen-specific Ige response by antibodies to C epsilon2 domain
A.Reference number: S34198
A.Accession: S34198
A.Molecule type: mRNA
A.Residues: 1-309 <FLIO>
A.Cross-references: EMBL:X73579; NID:9313672; PIDD:CAA51981.1; PID:9313673
C.Superfamily: Ige receptor II; C-type lectin homology
C.Keywords: B-cell; glycoprotein; immunoglobulin receptor; macrophage; tandem repeat; trypsin-sensitive; intracellular #status predicted <INT>
F:14-22/Region: stop-transfer sequence

F:124-46/Domain: extracellular #status predicted <TM>
F:47-309/Domain: extracellular #status predicted <EXT>
F:126-309/Product: soluble Ig9-binding factor (29K) #status predicted <IG1>
F:149-309/Product: soluble Ig9-binding factor (25-27K) #status predicted <BF1>
F:164-283/Domain: C-type lectin homology factor (IC9H) #status predicted <IC9H>
F:192-283,260-274/Disulfide bonds: #status predicted

	Query Match	16.1%	Score 205.5	DB 1	Length 309	
	Best Local Similarity	30.5%	Pred. No. 1,3e-10			
	Matches	53	Conservative	35	Mismatches	63
					Indels	23
					Gaps	8
QY	71	KYSOLLEKRTKELVHTTLECVK	---	NMPVEETAMSCCPKMKSFSSNCYFISTESAS	126	
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100		
Db	125	KSQGLNKRASDSLEKIQEEVAKLMIEILMSKGTACVNCPRDMLHFOOKCYVFEGSGKQ			184	
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100				
QY	127	WQDEKDCARNEAHLVINTQEEQDFITQNLQEEASATVYGLSDPSCGRHMOWDQTPYNE			186	
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100				
Db	185	WIOAKFTCSLDIEGRVLSHSQKEDDFLMQHTINKKESW-IGQDLMEEGEFVWPDSPGYX			243	
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100				
QY	187	SSTFMHPREPSD--PNERCVLVNFRSPKSPKMGVNVNLTGPORS-----VCEMM			233	
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100				
Db	244	SN--WNREPNNGGGGEGCVMM--RGSGQ-----WINDAFC-----KSLIDANVCEQL			286	
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100				

RESULT 15
A46274
HIV gp120-binding C-type lectin - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-1995
C:Accession: A46274
R:Curulis, B.M.; Scharnrowske, S.; Watson, A.J.
Proc. Natl. Acad. Sci. U.S.A. 89, 8356-8360, 1992
A:Title: Sequence and expression of a membrane-associated C-type lectin that exhibits
A:Reference number: A46274; MUID:92390446; PMID:11518869
A:Accession: A46274
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-404 <CUR>
A:Experimental source: Placenta
A:Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBITP:113135)
C:Superfamily: C-type lectin homology
C:Subfamily: C-type lectin homology <LCH>
J:256-377/Domain: C-type lectin homology

[illegible]

```
Search completed: August 4, 2003, 13:11:38
Job time : 41 secs
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